

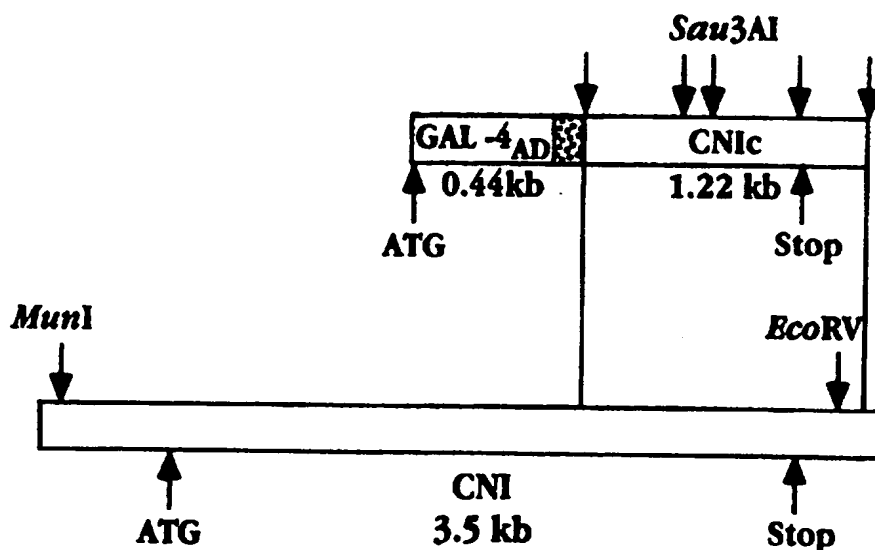


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**(54) Title:** CALCINEURIN INTERACTING PROTEIN COMPOSITIONS AND METHODS**(57) Abstract**

An identification and characterization of a calcineurin interacting (CNI) protein effective to enhance immunosuppressive effects of calcineurin-targeted immunosuppressants by potentiating an interaction of an immunophilin with calcineurin is described herein. One embodiment of the invention is the CNI polypeptide encoded by the *CNI* gene of *Saccharomyces cerevisiae*. Polynucleotides encoding a CNI protein are also described. Also described are yeast cells carrying mutations in the *CNI* gene. Further, a method of identifying a small molecule immunosuppressant compound is described. The methods include the use of a cell-based two hybrid protein-protein interaction assay, wherein one of two fusion hybrid proteins in a cell contains a subunit of calcineurin, and the other of two fusion hybrid proteins contains an immunophilin.



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**CALCINEURIN INTERACTING PROTEIN**  
**COMPOSITIONS AND METHODS**

**Field of the Invention**

- 5       The present invention relates to compounds affecting the function of calcineurin, particularly interactions of calcineurin with immunosuppressant drugs.

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### 30 Background of the Invention

The immune system functions as the body's major defense against diseases caused by invading organisms. This complex system fights disease by killing invaders such as bacteria, viruses, parasites or cancerous cells while leaving the body's normal tissues unharmed. The immune system's ability to distinguish the body's normal tissues, or self, from foreign or

cancerous tissue, or non-self, is an essential feature of normal immune system function. A second essential feature is memory, the ability to remember a particular foreign invader and to mount an enhanced defensive response when the previously encountered invader returns. The loss of recognition of a particular tissue as self and the subsequent immune response  
5 directed against that tissue produce serious illness.

An autoimmune disease results from the immune system attacking the body's own organs or tissues, producing a clinical condition associated with the destruction of that tissue. An autoimmune attack directed against the joint lining tissue results in rheumatoid arthritis; an attack against the conducting fibers of the nervous system results in multiple sclerosis. The  
10 autoimmune diseases most likely share a common pathogenesis and the need for safe and effective therapy. One type of therapy that has been employed in combating autoimmune disease is treatment with immunosuppressant drugs, such as cyclosporin A, FK506 and rapamycin. While the treatments are often effective, the drugs typically have undesirable side effects, including neurotoxicity, nephrotoxicity, hypertension, and metabolic disorder. Many  
15 of these side effects are due to the drugs' action on cells other than those of the immune system.

In addition to their use in treating autoimmune conditions, immunosuppressive agents have also been used in treating or preventing transplantation rejection. Organ transplantation involving human organ donors and human recipients (allogeneic grafts), and non-human  
20 primate donors and human recipients (xenogeneic grafts), has received considerable medical and scientific attention (*e.g.*, Roberts, 1989; Platt, 1990). To a great extent, this effort has been aimed at eliminating, or at least reducing, the problem of rejection of the transplanted organ. In the absence of adequate immunosuppressive therapy, the transplanted organ is destroyed by the host immune system.

Presently, the most commonly used agents for preventing transplant rejection include corticosteroids, cytotoxic drugs that specifically inhibit T cell activation such as azathioprine, immunosuppressive drugs such as cyclosporin A, and specific antibodies directed against T  
25 lymphocytes or surface receptors that mediate their activation (Briggs, 1991; Kennedy, 1983; Storb, 1985; Storb, 1986). All of these drug therapies are limited in effectiveness, in part  
30 because the doses needed for effective treatment of transplant rejection may increase the patient's susceptibility to infection by a variety of opportunistic invaders, and in part because of direct toxicity and other side effects.

Cyclosporin A, currently the most effective and most commonly used agent, is significantly toxic to the kidney. This nephrotoxicity limits the quantity of drug that can be

safely given. The physician is frequently forced to administer sub-optimal doses of the drug because of this toxicity. A preparation capable of potentiating the action of immunosuppressive agents such as cyclosporin A on the immune system, thus allowing the administration of lower doses of drug, would be of considerable value in reducing the morbidity and mortality associated with transplantation.

### **Summary of the Invention**

In one embodiment, the present invention includes polypeptide compositions effective to enhance immunosuppressive effects of calcineurin-targeted immunosuppressants by potentiating an interaction of an immunophilin with calcineurin. The present invention includes the isolation and characterization of a calcineurin interacting protein, CNI, having these properties. Also disclosed herein are methods for the isolation and characterization of further CNI-related sequences and sequences of CNI-variants. The amino acid sequences presented as SEQ ID NO:2 and SEQ ID NO:5 are exemplary of the polypeptides of the present invention.

The present invention also includes a CNI polypeptide fragment that interacts specifically with the "A" subunits of calcineurin (CNA1 and CNA2), but not with calcineurin "B" subunit (CNB1). In one embodiment, this fragment has an amino acid sequence of between 15 and 915 amino acids in length, for example, the c-terminal 306 amino acids of the CNI protein (CN1c).

Included aspects of the invention are an CNI polypeptide; a recombinant CNI polypeptide; and a fusion polypeptide comprised of an CNI polypeptide. Exemplary fusion proteins include fusions to  $\beta$ -galactosidase.

The invention further includes isolated nucleic acid sequences encoding the above described polypeptides and polypeptide fragments. Exemplary nucleic acid sequences include the sequences presented as SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4 and SEQ ID NO:6. The present invention includes CNI-encoding genomic polynucleotides, cDNAs thereto and complements thereof. With respect to polynucleotides, some aspects of the invention include: a purified CNI-encoding genomic polynucleotide; CNI polypeptide-encoding RNA and DNA polynucleotides; recombinant CNI polypeptide-encoding polynucleotides; a recombinant vector including any of the above recombinant polynucleotides, and a host cell transformed with any of these vectors. Another aspect of the invention is a polynucleotide probe for CNI polypeptide-encoding sequences.

Portions of a CNI-polypeptide coding sequences are effective as probes to isolate variants coding sequences which occur naturally, or to determine the presence of such coding

sequences in nucleic acid samples. Such probes include hybridization screening probes and polymerase chain reaction amplification primers specific for CNI-polypeptide coding sequences. Homologues of CNI may be isolated from a number of sources, such as other types of yeast cells (*e.g.*, *Schizosaccharomyces*) or mammalian cells (*e.g.*, human).

5 Other aspects of the invention include: a recombinant expression system which incorporates an open reading frame (ORF) derived from CNI polypeptide-encoding sequences, wherein the ORF is linked operably to a control sequence which is compatible with a desired host, a cell transformed with the recombinant expression system, and a polypeptide produced by the transformed cell. Typically the expression system includes a vector having (a) a nucleic  
10 acid containing an open reading frame that encodes a CNI-polypeptide; and (b) regulatory sequences effective to express said open reading frame in a host cell. The regulatory sequence may include sequences useful for targeting or secretion of the CNI-polypeptide: such as a secretory signal recognized in yeast or bacterial expression systems.

The invention includes a method of recombinantly producing CNI-polypeptides. In the  
15 method, a recombinant expression system containing an open reading frame (ORF) having a polynucleotide sequence which encodes a CNI-polypeptide, where the vector is designed to express the ORF in the host, is introduced into suitable host cells. The host is then cultured under conditions resulting in the expression of the ORF sequence. The CNI-polypeptide sequences discussed above are examples of suitable CNI-polypeptides. Numerous vectors and  
20 their corresponding hosts are useful in the practice of this method of the invention, including, but not limited, to the vectors described herein for expression in yeast cells, and lambda gt11 phage vector and *E. coli* cells. Other host cells include insect and mammalian cell expression systems.

The invention also includes purified antibodies that are immunoreactive with a CNI-  
25 polypeptide. The antibodies may be polyclonal or monoclonal. Antibodies that are specifically immunoreactive with CNI-polypeptides may be useful for the isolation of CNI-polypeptide homologues from other cell type sources (*e.g.*, mammalian).

The present invention also includes, a method of identifying a small molecule immunosuppressant compound. In the method, a cell-based two hybrid protein-protein  
30 interaction assay is constructed where one of two fusion hybrid proteins in the cell contains a subunit of calcineurin, and the other of two fusion hybrid proteins contains an immunophilin. The cell is then contacted with the small molecule being tested. A small molecule is identified as an immunosuppressant if the molecule potentiates an interaction between the two hybrid proteins. In one embodiment, the method is carried out using yeast cells, where one of the two

fusion hybrid proteins contains a GAL4 activation domain and the other of two fusion hybrid proteins contains a GAL4 binding domain. The method can be carried out where subunits of calcineurin are from any cell source, in particular, yeast or mammalian cells (including human cells). The subunit may, for example, be yeast calcineurin subunit CNA1 or CNA2, or human  
5 calcineurin subunit "A". The immunophilin can, for example, be cyclophilins or FK506-binding proteins (*e.g.*, FKBP12) typically from a homologous cell source.

Also included in the present invention is another method of identifying a small molecule immunosuppressant compound. In the method, a cell-based two hybrid protein-protein interaction assay is constructed, wherein one of two fusion hybrid proteins in a cell contains  
10 an "A" subunit of calcineurin, and the other of two fusion hybrid proteins contains a CNI polypeptide. The cell preferably, but not necessarily, also contains a vector construct causing overexpression, or increased expression, of a "B" subunit of calcineurin. The cell is then contacted with the small molecule being tested. A small molecule is identified as an immunosuppressant if the molecule potentiates an interaction between the two hybrid proteins.  
15 This method is used to identify compounds (like FK506) that potentiate the interaction between CNI and CNA1. In one embodiment, the method is carried out using yeast cells, where one of the two fusion hybrid proteins contains a GAL4 activation domain and the other of two fusion hybrid proteins contains a GAL4 binding domain. The method can be carried out where subunits of calcineurin are from any cell source, in particular, yeast or mammalian cells  
20 (including human cells). The subunits may, for example, be calcineurin subunit A1 or A2. The CNI polypeptide may also be from any source (*e.g.*, yeast or human), and may be only a fragment of a complete CNI polypeptide (such as a c-terminal fragment). An exemplary c-terminal fragment of CNI is CN1c.

Further, included in the present invention, is a yeast cell carrying a mutation in the  
25 naturally-occurring copy of *CNI*, where the mutation prevents expression of a functional CNI protein from the genomic copy. Embodiments of this aspect of the present invention include deletion mutations within the coding region of the *CNI* gene, deletion of regulation regions of the *CNI* gene, and non-sense or mis-sense mutations in the *CNI* gene. Yeast cells having such mutations are useful, for example, in a method of identifying proteins of similar function to  
30 CNI. In one embodiment, a hybrid interaction screen is set up in a cell with a CNI deletion and a GAL4 protein binding domain-CNA fusion and a GAL4 activation domain-immunophilin fusion. Expression libraries are then screened to identify clones encoding proteins that potentiate an interaction of an immunophilin with calcineurin. This screen will identify CNI-coding sequences as well as other proteins with a similar function.



In a related embodiment, a yeast cell with a CNI deletion is used to identify CNI homologues (*e.g.*, from other organisms, such as human) using a complementation assay or screen. Expression libraries (*e.g.*, human lymphocyte expression libraries) are transformed into cells with a CNI deletion, and transformants are selected on their ability to complement the function of yeast CNI. An exemplary assay for selecting such transformants is exposure to hygromycin B. Cells which become more sensitive to hygromycin B following transformation are further analyzed to determine if the plasmid with which they were transformed contains an insert homologous to yeast CNI, or encoding a polypeptide with similar function to CNI.

The invention also includes a yeast cell carrying a mutation in the naturally-occurring genomic copy of a gene encoding calcineurin-interacting polypeptide, where the mutation prevents expression of a functional calcineurin-interacting polypeptide from the genomic copy. The mutation may be a null mutation, such as described in Example 8 below, or a different type of mutation, *e.g.*, a nonsense or missense mutation. Nonsense and missense mutations may be generated using standard methods.

These and other objects and features of the invention will be more fully appreciated when the following detailed description of the invention is read in conjunction with the accompanying drawings.

#### **Brief Description of the Figures**

Figures 1A and 1B present schematic diagrams of sequences encoding the c-terminal portion of CNI (CN1c) fused to GAL-4 activation domain (GAL-4AD) (Fig. 1A), and sequences encoding CNI (Fig. 1B).

Figure 2A presents data from a  $\beta$ -galactosidase ( $\beta$ -gal) assay to detect the interaction of CN1c with the A1 subunit of calcineurin (CNA1), A2 subunit of calcineurin (CNA2), GAL-4 binding domain (G4BD) and lamin C. A labeled schematic diagram corresponding to the data shown in Fig. 2A is presented in Fig. 2B to facilitate reference to individual groups of colonies.

Figure 3A presents data from a  $\beta$ -gal assay to detect the interaction of CN1c with CNA1 $\Delta$ C, CNA2 $\Delta$ C and CNB1. A labeled schematic diagram corresponding to the data shown in Fig. 3A is presented in Fig. 3B.

Figures 4A and 4C present data from  $\beta$ -gal assays to evaluate the effects of FK506 and the deletion of CNB1 on the interactions of CN1c with CNA and CNA $\Delta$ C. Labeled schematic diagrams corresponding to the data shown in Figs. 4A and 4C are presented in Figs. 4B and 4D, respectively.

Figures 5A and 5C present data from  $\beta$ -gal assays to evaluate the effects of FK506 and the overexpression of CNB1 on the interactions of CN1c with CNA and CNA $\Delta$ C. Labeled schematic diagrams corresponding to the data shown in Figs. 5A and 5C are presented in Figs. 5B and 5D, respectively.

- 5        Figures 6A, 6C and 6E present data from  $\beta$ -gal assays to evaluate the effects of FK506, cyclosporin A (CsA), and the deletion of CNB1 on the interaction of CN1c with CNA and CNA $\Delta$ C. Labeled schematic diagrams corresponding to the data shown in Figs. 6A, 6C and 6E are presented in Figs. 6B, 6D and 6F, respectively.

- 10       Figures 7A, 7C, 7E and 7G present data from  $\beta$ -gal assays to evaluate the effects of FK506, cyclosporin A (CsA), rapamycin and the overexpression of CNB1 on the interaction of CN1c with CNA and CNA $\Delta$ C. Labeled schematic diagrams corresponding to the data shown in Figs. 7A, 7C, 7E and 7G are presented in Figs. 7B, 7D, 7F and 7H, respectively.

- 15       Figure 8A presents data from a  $\beta$ -gal assay to evaluate the effects of overexpression of full-length CNI on FK506-dependent interaction of FKBP with CNA. A labeled schematic diagram corresponding to the data shown in Fig. 8A is presented in Fig. 8B.

Figures 9A and 9C present data from  $\beta$ -gal assays to evaluate the effects of overexpression of full-length CNI on FK506-dependent interaction of FKBP with CNB1. Labeled schematic diagrams corresponding to the data shown in Figs. 9A and 9C are presented in Figs. 9B and 9D, respectively.

- 20       Figure 10 presents an image of a protein blot of CN1c and CNA co-immunoprecipitate probed with anti-CNA2 antibody.

Figure 11 presents an image of a yeast RNA blot hybridized with a CN1c probe.

Figure 12 presents the DNA sequence of a 3.5 kb fragment of yeast chromosome 11 containing the coding sequence for a yeast CNI protein.

- 25       Figure 13 presents the amino acid sequence of a yeast CNI protein.

#### **Brief Description of the Sequences**

SEQ ID NO:1 presents the nucleotide sequence of a *Sau3AI* fragment containing the coding sequence for CN1c.

- 30       SEQ ID NO:2 presents the amino acid sequence of CN1c encoded by SEQ ID NO:1.

SEQ ID NO:3 presents the coding sequence presented in SEQ ID NO:1.

SEQ ID NO:4 presents the nucleotide sequence of a gene encoding a complete CNI protein.

SEQ ID NO:5 presents the amino acid sequence encoded by SEQ ID NO:4.

SEQ ID NO:6 presents the coding sequence presented in SEQ ID NO:4.

SEQ ID NO:7 presents the nucleotide sequence of PCR primer CNI-PCR-A.

SEQ ID NO:8 presents the nucleotide sequence of PCR primer CNI-PCR-B.

5     SEQ ID NO:9 presents the nucleotide sequence of a gene encoding the yeast CNA1 subunit of calcineurin.

SEQ ID NO:10 presents the amino acid sequence encoded by SEQ ID NO:9.

SEQ ID NO:11 presents the nucleotide sequence of a gene encoding the yeast CNA2 subunit of calcineurin.

SEQ ID NO:12 presents the amino acid sequence encoded by SEQ ID NO:11.

10     SEQ ID NO:13 presents the nucleotide sequence of a gene encoding the yeast CNB1 subunit of calcineurin.

SEQ ID NO:14 presents an amino acid sequence encoded by SEQ ID NO:13.

SEQ ID NO:15 presents an amino acid sequence encoded by SEQ ID NO:13.

SEQ ID NO:16 presents the coding sequence presented in SEQ ID NO:13.

15     SEQ ID NO:17 presents the amino acid sequence encoded by SEQ ID NO:16.

SEQ ID NO:18 presents a nucleotide sequence encoding CNA1Δc.

SEQ ID NO:19 presents the amino acid sequence encoded by SEQ ID NO:18.

SEQ ID NO:20 presents a nucleotide sequence encoding CNA2Δc.

SEQ ID NO:21 presents the amino acid sequence encoded by SEQ ID NO:20.

20     SEQ ID NO:22 presents the nucleotide sequence of PCR primer G4-PCR-A.

SEQ ID NO:23 presents the nucleotide sequence of PCR primer G4-PCR-B.

### **Detailed Description of the Invention**

#### **I. DEFINITIONS**

25     A "calcineurin-targeted immunosuppressant" is a compound that possesses *in vivo* immunosuppressive activity, and that interacts with an immunophilin to form a complex which is capable of inhibiting calcineurin.

"Interacting proteins" are proteins capable of specifically binding to one another, or associating with one another, in a cell or *in vitro*.

30     A calcineurin interacting (CNI) protein or polypeptide is a protein or polypeptide that is effective to enhance immunosuppressive effects of a calcineurin-targeted immunosuppressant by potentiating an interaction of an immunophilin with calcineurin. Preferably, a CNI protein or polypeptide is a protein or polypeptide having an amino acid sequence that is homologous to the sequence presented herein as SEQ ID NO:5.

"Substantially isolated" is used in several contexts and typically refers to the at least partial purification of a CNI protein or polypeptide fragment away from unrelated or contaminating components (*e.g.*, cytoplasmic contaminants and heterologous proteins). Methods and procedures for the isolation or purification of compounds or components of interest are described below (*e.g.*, affinity purification of fusion proteins and recombinant production of CNI polypeptides).

In the context of the present invention, the phrase "nucleic acid sequences," when referring to sequences which encode a protein, polypeptide, or peptide, is meant to include degenerative nucleic acid sequences which encode homologous protein, polypeptide or peptide sequences as well as the disclosed sequence.

Two nucleic acid fragments are considered to have "homologous" sequences if they are capable of hybridizing to one another (i) under typical hybridization and wash conditions, as described, for example, in Sambrook, *et al.*, pages 320-328, and 382-389, or (ii) using reduced stringency wash conditions that allow at most about 25-30% basepair mismatches, for example: 2 × SSC, 0.1% SDS, room temperature twice, 30 minutes each; then 2 × SSC, 0.1% SDS, 37°C once, 30 minutes; then 2 × SSC, room temperature twice, 10 minutes each. Preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches. These degrees of homology can be selected by using wash conditions of appropriate stringency for identification of clones from gene libraries (or other sources of genetic material), as is well known in the art.

Two amino acid sequences or two nucleotide sequences (in an alternative definition for homology between two nucleotide sequences) are considered homologous (as this term is preferably used in this specification) if they have an alignment score of >5 (in standard deviation units) using the program ALIGN, typically default mutation gap matrix and gap penalty (Dayhoff). The two sequences (or parts thereof) are more preferably homologous if their amino acids are greater than or equal to 40% using the ALIGN program mentioned above.

## II. OVERVIEW OF INVENTION

Experiments performed in support of the present invention demonstrate the identification and isolation of the nucleic acid sequence encoding a calcineurin interacting (CNI) protein. Further experiments performed in support of the present invention characterize the CNI protein, as well as a polypeptide containing only the c-terminal 306 amino acids of the CNI protein (CN1c). The experiments demonstrate that CN1c interacts specifically with the "A" subunits of calcineurin (CNA1 and CNA2), but not with calcineurin "B" subunit (CNB1).

The experiments also demonstrate that CN1c does not interact directly with FK506 binding protein (FKBP; Schreiber, *et al.*; with or without FK506), GAL4 binding domain (G4<sub>BD</sub>) or lamin C. The experiments also demonstrate that CN1c interacts with C-terminally truncated forms of CNA (CNA $\Delta$ C), which have lost their autoinhibitory domains, though the interaction  
5 is somewhat weaker than with full length CNA proteins.

Additional experiments show that the interaction between CN1c and CNA is enhanced when CNB1 is deleted, and diminished when CNB1 is overexpressed, that the interaction between CN1c and CNA or CNA $\Delta$ C is markedly enhanced by FK506 and by Cyclosporin A (CsA), but not rapamycin, and that overexpression of a full-length CNI protein enhances the  
10 interaction between CNA and FKBP (detectable only in the presence of FK506).

Additional experiments conducted in support of the present invention demonstrate that overexpression of the full-length CNI has no detectable effect on the interaction between CNB1 and CNA, and that in the presence of FK506 or CsA, overexpression of CNB1 no longer inhibits the interaction of CN1c with CNA.

15 It was also found that CNI deletion mutants are viable, both in wild-type and CN-deletion backgrounds, and that CNI deletion mutants in a CN-deletion background are more resistant to hygromycin B than normal CN-deletion mutants.

Co-immunoprecipitation experiments demonstrate that CN1c and CNA co-immunoprecipitate in the presence of FK506, and protein blot experiments show that CNI is expressed at  
20 low levels *in vivo*. RNA blot experiments show that CNI is encoded by a single message approximately 2.9 kb in length.

A comparison of the yeast CNI sequence with sequences present in nucleic acid and amino acid databases reveals no obvious homologous sequences have been identified in other  
25 organisms.

### III. CALCINEURIN

Experiments performed in support of the present invention were designed to identify polypeptides capable of interacting with calcineurin. Calcineurin (also called phosphoprotein phosphatase 2B or PP2B), has been characterized from many different tissues and organisms  
30 (Klee, *et al.*). It is a heterodimer of two subunits, of which the "A" subunit is about 61 kD in weight, possesses catalytic activity and also contains the association site for calmodulin. The "B" subunit contains four Ca<sup>2+</sup> binding sites and activates the A subunit. Calcineurin has little enzymatic activity, even in the presence of Ca<sup>2+</sup> and only becomes fully active when associated with calmodulin (Cyert).

Two A subunits (CNA1 and CNA2; Cyert, *et al.*, 1991) and one B subunit (CNB1, Cyert, *et al.*, 1992) have been cloned in yeast. Either CNA1 or CNA2 may associate with CNB1 to form a functional calcineurin heterodimer. Multiple isotypes of the A subunit have been cloned from a variety of organisms and are highly conserved (Klee, *et al.*). In particular, 5 calcineurin subunits have been cloned from human tissue (see reviews by, for example, Klee, *et al.*, and Guerini, *et al.*).

#### IV. IMMUNOSUPPRESSANT DRUGS

FK506, cyclosporin A (CsA) and rapamycin, derived from fungi, inhibit the activation 10 of T-cells by antigens. The compounds have proven highly effective at suppressing mammalian immune systems *in vivo*. In particular, CsA therapy in clinical settings has dramatically increased the success rate of transplantation therapy.

It is now known that FK506 and CsA exert their immunosuppressive effects, in part, by inhibiting the transcriptional activation of the interleukin-2 (IL-2) gene, whereas rapamycin 15 appears to function by inhibiting the response of T-cells to IL-2, presumably by inhibiting a transduction pathway mediated by the IL-2 receptor.

The molecular mechanism of FK506 and CsA immunosuppressive action involves a group of small, abundant intracellular proteins termed immunophilins, which bind with a high affinity to the immunosuppressants (Schreiber). At least two classes of immunophilins are 20 known to exist. One class, termed cyclophilins, binds to CsA, while another class, the FK506-binding proteins (FKBPs) binds FK506 and rapamycin. Many immunophilin genes, from a variety of organisms, have been cloned, and appear to be highly conserved from simple eukaryotes to mammals.

It is believed that FK506 and CsA-induced immunosuppression is due to the binding 25 of complexes, formed by binding of immunosuppressants FK506 and CsA bound to one of their respective immunophilins, to the catalytic subunit of calcineurin (Schreiber, *et al.*, Liu, *et al.*, Foor, *et al.*, Weiss, *et al.*). The binding of such a complex to an (A) subunit inhibits activation of calcineurin by increased intracellular calcium, which in turn prevents calcineurin from activating transcription factor NF-AT. Since IL-2 is one of the genes controlled by NF- 30 AT in T-cells, inhibition of the transcription factor inhibits the production of IL-2, resulting in immunosuppression (Clipstone, *et al.*).

FK506 and CsA are widely used in organ transplantation to prevent host rejection. However, both drugs are known to have many undesired side-effects such as neurotoxicity, nephrotoxicity, hypertension, and metabolic disorder. Accordingly formulations effective to

increase a target cell's sensitivity to these drugs may be useful in alleviating some of the aforementioned side-effects. Specifically, CNI and its homologues or derivatives, administered at appropriate levels, may be able to increase the sensitivity of CN to FK506/CsA and reduce the necessary dosage thus reducing or eliminating the side-effects of these drugs.

5

#### V. TWO HYBRID PROTEIN INTERACTION ASSAYS

Two hybrid protein interaction assay methods (two hybrid protein-protein interaction screens) provide a simple and sensitive means to detect the interaction between two proteins in living cells. The assays are based on the finding that most eukaryotic transcription activators  
10 are modular (e.g, Brent, *et al.*), *i.e.*, that the activators typically contain activation domains that activate transcription, and DNA binding domains that localize the activator to the appropriate region of a DNA molecule.

The development of two hybrid protein interaction assays was made possible by the observation that the DNA binding domain does not need to be physically located on the same  
15 polypeptide as the activation domain (Ma, *et al.*, Triezenberg, *et al.*), raising the possibility that transcription of reporter genes could be used as an assay to detect protein interactions.

The utility of two hybrid systems for detecting interactions between two interacting proteins was fully realized by the observation that protein interactions could be detected if two potentially-interacting proteins were expressed as fusions, or chimeras (Fields, *et al.*). A first  
20 fusion protein contains one of a pair of interacting proteins fused to a DNA binding domain, and a second fusion protein contains the other of a pair of interacting proteins fused to a transcription activation domain. The two fusion proteins are independently expressed in the same cell, and interaction between the "interacting protein" portions of the fusions reconstitute the function of the transcription activation factor, which is detected by activation of  
25 transcription of a reporter gene.

At least two different cell-based two hybrid protein-protein interaction assay systems have been used to assess binding interactions and/or to identify interacting proteins. Both employ a pair of fusion hybrid proteins, where one of the pair contains a first of two  
30 "interacting" proteins fused to a transcription activation domain of a transcription activating factor, and the other of the pair contains a second of two "interacting" proteins fused to a DNA binding domain of a transcription activating factor.

The yeast GAL4 two hybrid system (Fields, *et al.*, Chien, *et al.*, Durfee, *et al.*, Bartel, *et al.*), utilized for experiments performed in support of the present invention, was developed

to detect protein-protein interaction based on the reconstitution of function of GAL4, a transcriptional activator from yeast, by activation of a *GAL1-lacZ* reporter gene.

Like several other transcription activating factors, GAL4 contains two distinct domains, a DNA binding domain and a transcription activation domain. Each domain can be independently expressed as a portion of a fusion protein composed of the domain, and a second, "bait" interacting protein. The two fusion proteins are then independently expressed together in a cell. When the two GAL4 domains are brought together by a binding interaction between the two "interacting" proteins, transcription of a reporter gene under the transcriptional control of GAL4 is initiated. The reporter gene typically has a promoter containing GAL4 protein binding sites (GAL upstream activating sequences, UAS<sub>G</sub>). Exemplary reporter genes are the *GAL1-lacZ*, and *GAL1-HIS3* reporter genes used in experiments described herein.

A second two hybrid system, described in detail in Ausubel, *et al.*, utilizes a native *E. coli* LexA repressor protein, which binds tightly to appropriate operators. A plasmid is used to express one of a pair of interacting proteins (the "bait" protein) as a fusion to LexA. The plasmid expressing the LexA-fused bait protein is used to transform a reporter strain of yeast, such as EGY48, that contains pSH18-34.

In this strain, binding sites for LexA are located upstream of two reporter genes. In the first reporter system, the upstream activation sequences of the chromosomal LEU2 gene—required in the biosynthetic pathway for leucine (Leu)—are replaced in EGY48 with *lexA* operators, permitting selection for viability when cells are plated on medium lacking Leu. In the second reporter system, EGY48 harbors a plasmid, pSH18-34, that contains a *lexA* operator-*lacZ* fusion gene, permitting discrimination based on color when the yeast is grown on medium containing Xgal (Ausubel, *et al.*).

To screen a library with the LexA system, the library uses the inducible yeast GAL1 promoter to express proteins as fusions to an acidic domain ("acid blob") that functions as a portable transcriptional activation motif ("act"), and to other useful moieties. Expression of library-encoded proteins is induced by plating transformants on medium containing galactose (Gal), so yeast cells containing library proteins that do not interact specifically with the bait protein fail to grow in the absence of Leu. Yeast cells containing library proteins that interact with the bait protein form colonies within 2 to 5 days, and the colonies turn blue when the cells are streaked on medium containing Xgal. The plasmids are isolated and characterized by a series of tests to confirm specificity of the interaction with the initial bait protein. Those found to be specific are ready for further analysis (e.g., sequencing).



LexA and GAL4 each have different properties that should be considered when selecting a system. LexA is derived from a heterologous organism, has no known effect on the growth of yeast, possesses no residual transcriptional activity, can be used in GAL4<sup>+</sup> yeast, and can be used with a Gal-inducible promoter. Because GAL4 is an important yeast transcriptional activator, experiments must be performed in *gal4* yeast strains to avoid background from endogenous GAL4 activating the reporter system.

Both two hybrid systems have been successfully used for isolating genes encoding proteins that bind a target protein and as simple protein binding assays (*e.g.*, Yang, *et al.*, Gyuris, *et al.*), and both can be applied to methods of the present invention.

Both gene isolation and protein binding assay applications of the GAL4 system are described in Examples below.

#### VI. SPECIFIC EMBODIMENTS

Example 1 demonstrates application of an exemplary two hybrid protein-protein interaction screen (Materials and Methods, section D) to the screening of three pGAD yeast fusion libraries, carrying fusions between the transcription activating domain of yeast protein GAL4 (G4AD) and yeast genomic DNA *Sau3A*I fragments, in all three reading frames. The libraries are screened to identify polypeptides, encoded by the *Sau3A*I fragments, capable of interacting with catalytic (A) subunits of calcineurin, expressed as fusions with the GAL4 protein binding domain (GBT-CNA fusions).

Three sets of yeast cells harboring pGBT-CNA1 *TRP1* (GBT-A1) hybrid plasmid and a GAL4-activated LacZ reporter gene are each transformed with one of the three reading-frame libraries. Construction of the plasmids used is described in Materials and Methods, sections B and C. Cells transformed with a plasmid encoding a protein fusion capable of interacting with the CNA subunit fusion are selected using a  $\beta$ -galactosidase ( $\beta$ -gal) assay on plates containing the chromogenic substrate X-gal (Materials and Methods, section E). Results of the  $\beta$ -gal assay are confirmed using a growth assay (Materials and Methods, section F). False positives are eliminated by colony purification (re-streaking for single colonies), PCR experiments using GAL4 primers, and testing against a number of test fusions by  $\beta$ -gal assays on transformed haploid or mated diploid reporter strains.

A yeast clone encoding a polypeptide capable of specifically interacting with CNA polypeptide fusions is identified and sequenced. The sequence of the *Sau3A*I fragment is presented as SEQ ID NO:1. The coding sequence forming the open reading frame is presented as SEQ ID NO:3. The polypeptide encoded by the open reading frame is presented as SEQ

ID NO:2. The open reading frame encodes 306 amino acids followed by a stop codon in frame with the coding sequence of GAL4, but does not contain an in-frame ATG start site upstream of the stop codon. This is consistent with the fragment encoding a c-terminal portion of a complete gene product. The clone is termed CN1c, with the lowercase "c" representing "c-terminal".

Figure 1A shows a schematic representation of the nucleic acid sequence encoding the GAL4AD-CN1c fusion protein. The stippled portion between GAL4AD and CN1c represents a linker discussed in the Materials and Methods section, as well as in Example 1. Also indicated in the Figure are the approximate locations of in-frame start (ATG) and stop codons, and *Sau3AI* restriction sites.

Example 1 further describes the identification of a  $\lambda$  clone encoding a full length sequence version of CN1c, termed CN1. The polypeptide encoded by the sequence is termed CN1 protein. The clone is identified by hybridization screening of a panel of  $\lambda$  clones spanning the yeast genome using a 1.22 kb  $^{32}\text{P}$ -labeled probe generated from CN1c.

Phage lysates of the  $\lambda$  clone are amplified, purified, restriction-mapped and used as a DNA source for subsequent cloning experiments. A 3.16 kb *MunI/EcoRV* fragment from the  $\lambda$  clone insert contains the coding sequence of CN1. The sequence of the 3.16 kb *MunI/EcoRV* fragment is encompassed by the 3.5 kb sequence presented as SEQ ID NO:4, and a schematic diagram of the sequence is shown in Figure 1B. This sequence contains the entire 2.75 kb coding sequence of CN1 (SEQ ID NO:6; graphically indicated in Figure 1B by the locations of the "ATG" and "Stop" codons).

A search of known DNA and protein sequences turns up no obvious matches or homologies to genes in other organisms. Accordingly, CN1 may represent a new type of calcineurin interacting protein.

The methods referred to above may also be applied to the screening of, for example, a human cDNA library using an appropriate two-hybrid protein interaction screen. The "bait" protein in the interaction screen (*e.g.*, the protein analogous to CNA1 in Example 1) may be of yeast origin (*e.g.*, CNA1), but is preferably of human origin (*e.g.*, a human calcineurin "A" subunit; Klee, *et al.*). The bait protein is expressed in the cell (*e.g.*, a yeast cell) used for the two hybrid interaction screen as a fusion to a domain of a transcription activating factor (*e.g.*, the DNA binding domain of GAL4). The library may be a human DNA library in a vector (*e.g.*, pGAD) effective to express library sequences as fusions to a complimentary domain of the transcription activating factor (*e.g.*, the activation domain of GAL4). Libraries of human sequences can be derived from a number of sources including genomic DNA, such as yeast

artificial chromosome (YAC) constructs carrying genomic human DNA, or cDNA generated from a variety of cell types (*e.g.*, activated T-cells).

Example 2 details a  $\beta$ -gal assay to determine the specificity of binding of CN1c to subunits of calcineurin. Exemplary results are shown in Figure 2A. The legend for Fig. 2A is shown in Figure 2B. Numbers in the legend refer to locations of yeast colonies expressing particular combinations of plasmid constructs (indicated in Example 2).

A comparison of the intensities of the blue  $\beta$ -gal reaction product indicates that CN1c interacts strongly with CNA1 (21, 22 and 23), and somewhat less strongly with CNA2 (24). Neither cells containing AS-lamin with GAD-CN1c (25), nor cells containing only GBT with GAD-CN1c (26) show a detectable signal above background. Two subunits of calcineurin (CNA1, CNB1) known to interact with each other are used as a positive control for the assay (20). The data presented in Figure 2A show that CN1c interacts specifically with CNA1 and CNA2, but not with G4BD or lamin C.

A similar set of experiments, illustrated in Fig. 3A, is conducted using constitutively-active CNA subunits, as well as calcineurin subunit CNB1. As described in the Materials and Methods section below, CNA1 $\Delta$ C and CNA2 $\Delta$ C are each missing a C-terminal portion of the protein containing an autoinhibitory domain. Exemplary results from these experiments are shown in Figure 3A. The legend for Fig. 3A is shown in Figure 3B. The data show that GBT-A1 $\Delta$ C and GAD-CN1c (28) gives a definite positive signal, while GBT-A2 $\Delta$ C and GAD-CN1c (29) is weaker, though still detectable above its background (*i.e.* GBT-A2 $\Delta$ C and GAD; 31). The signal from GBT-B1 and GAD-CN1c (32) is not detectable above vector background (GBT-B1 and GAD; 33). Positive controls GBT-A1 $\Delta$ C and GAD-B1 (34) and GBT-A2 $\Delta$ C and GAD-B1 (35) give strong signals. The data presented in Figure 3A show that CN1c interacts specifically with CNA1 $\Delta$ C and CNA2 $\Delta$ C, but not with CNB1.

Example 3 details the effects of immunosuppressant drugs on binding of CN1c to calcineurin in B1<sup>+</sup>, B1 Deletion and B1 Overproducing Yeast Strains. The yeast strains are assayed for  $\beta$ -gal activity as above to determine if the immunosuppressant drugs FK506, cyclosporin A (CsA) and rapamycin affect the binding of CN1c to subunits of calcineurin. The experiments are performed in yeast strains wild-type for the CNB1 subunit, null for the CNB1 subunit, and in yeast transformed with a high efficiency expression vector containing DNA encoding the CNB1 subunit.

Exemplary data are shown in Figures 4A, 4C, 5A and 5C. The legends for Figs. 4A and 4C are shown in Figures 4B and 4D, respectively. Figs. 4A and 5A illustrate experiment

performed without FK506, while experiments shown in Figs. 4C and 5C were performed with FK506.

The interactions of various combinations of proteins expressed by constructs indicated in Example 3 was studied in three yeast strains, one of which is null for the CNB1 subunit of calcineurin (Y153b; at 36-40), while the others (Y190; at 41-46 and Y526 at 47-51) are wild-type for CNA1, CNA2 and CNB1.

The data, shown in Fig. 4A (no added drugs), illustrate that deleting the endogenous host CNB1 gene potentiates, or enhances, interactions between CN1c and calcineurin subunits CNA1, CNA2, CNA1ΔC and CNA2ΔC. Comparison of corresponding colonies in Figs. 4A and 4C shows the effects of FK506 on CN1c-CNA/CNAΔC interactions. The drug enhances interactions under all except control conditions. The effect is most striking in yeast strains wild-type for the CNB1 subunit (*e.g.*, compare 50a with 50b, and 51a with 51b).

The drug also markedly enhances, or potentiates CN1c-CNA/CNAΔC interactions under conditions where the CNB1 subunit is overexpressed. Figure 5A shows the effect of overexpressing CNB1 on CN1c-CNA/CNAΔC interactions in the absence of drug. Colonies expressing B1/YEp352 (53a, 55a-58a) have reduced signal as compared with controls expressing only YEp352 (52a, 54a). Inclusion of FK506 in the plating medium (Fig. 5C), however, enhances, or potentiates interactions in all colonies, except the negative controls (56).

The data presented in Figures 4A, 4C, 5A and 5C demonstrate that the interaction of CN1c with CNA and CNAΔC is markedly enhanced by FK506. The interaction is also enhanced by deletion of CNB1 and diminished by overexpression of CNB1, and the inhibitory effect of CNB1 overproduction is overcome by the stimulatory effect of FK506.

Stated another way, inclusion of a small molecule immunosuppressant (FK506) potentiates an interaction between two fusion hybrid proteins, where one of the two proteins contains an (A) subunit of calcineurin, and the other protein contains a CNI polypeptide. The potentiation is particularly strong when the cell is further modified to cause overexpression of a "B" subunit of calcineurin by said cell (*e.g.*, the expresses B1/YEp352).

In the present case, a yeast cell is modified to cause overexpression of a "B" subunit of calcineurin (CNB1) by transforming the cell with B1/YEp352 (construction described below). A cell may be modified to cause overexpression of a "B" subunit of calcineurin in other ways as well, such as, for example, transformation with other types of expression vectors encoding a "B" subunit of calcineurin, or treatment with a substance that upregulates a promoter controlling expression of an endogenous (B) subunit of calcineurin.

In light of the effects of FK506 on CN1c-CNA/CNA $\Delta$ C interactions, two other immunosuppressants, cyclosporin A and rapamycin, were examined in similar experiments. The results of these experiments are shown in Figures 6A-6F and 7A-7H.

5 The data presented in Figures 6A and 6C are essentially equivalent to those presented in Figures 4A and 4C, respectively. Data shown in Figure 6E demonstrate that like FK506, the immunosuppressant cyclosporin A is also effective to enhance interaction of CN1c with CNA and CNA $\Delta$ C. Both FK506 and cyclosporin A are known to exert their immunosuppressive effects through calcineurin (Cyert).

10 Similarly, data shown in Figures 7A and 7C support data in Figures 5A and 5C, and further, demonstrate that there is no detectable interaction between FK506 binding protein (FKBP) and CN1c. Results shown in Fig. 7E demonstrate that cyclosporin A has a similar effect to FK506 in cells overexpressing CNB1 — that is, it enhances the interactions between CN1c and CNA/CNA $\Delta$ C.

In contrast, data presented in Fig. 7G show that the immunosuppressant rapamycin has 15 no detectable effect on CN1c-CNA/CNA $\Delta$ C interactions (compare Fig. 7G with Fig. 7A).

Taken together, the data presented in Figs. 6A, 6C, 6E 7A, 7C, 7E and 7G show that like FK506, cyclosporin A (CsA), but not rapamycin, enhances the interaction of CN1c with CNA and CNA $\Delta$ C, and that CN1c doesn't interact with FKBP with or without FK506.

20 Example 4 describes experiments to assess effects of CN1c on FKBP/FK506 binding to calcineurin. Figure 8A presents exemplary data from studies to assess the effect of CN1 on FKBP-mediated FK506 interactions with CNA2. The legend for Fig. 8A is shown in Figure 8B. Data in Figure 8A demonstrate that, in the absence of FK506, FKBP and CNA2 show no detectable interaction (84). In the presence of FK506, however, the proteins interact (85), presumably because FK506 forms a complex with FKBP, which then binds CNA2 (Cyert).

25 Data in Figure 8A further show that, in the absence of FK506, CN1 has no effect on the lack of interaction between FKBP and CNA2 (86). In the presence of FK506 (87), however, CN1 potentiates, or enhances the binding between FKBP and CNA2 (compare the intensity at 87 with that at 85). This effect suggests that CN1 and similar compounds may be employed to increase the sensitivity of calcineurin to immunosuppressant drugs that act on it, 30 and in this way, decrease the amount of the immunosuppressant required for a particular level of immunosuppression.

Experiments illustrated in Figures 9A and 9B demonstrate that FK506 has little or no effect on the binding of CNA to CNB1. The legends for Fig. 9A and 9B are shown in Figures 9B and 9D, respectively. The data in Fig. 9A show that overexpression of the full-length CN1

clone markedly enhances the FK506-dependent interaction of FKBP with CNA, although it doesn't affect the interaction between CNA and CNB1.

Example 5 presents co-immunoprecipitation of CN1c (carrying an HA epitope tag) and CNA. Immunoprecipitation is carried out with anti- HA monoclonal antibody and the immune complex, resolved by SDS-PAGE, is detected with anti-CNA2 polyclonal antibody and visualized with goat anti-rabbit antibody using the "ECL" method (Amersham, Arlington Heights, IL). The results, shown in Figure 10, demonstrate that CN1c is capable of binding to CNA2 tightly enough for the complex to be co-immunoprecipitated. Similar methods may be employed to isolate a CNI analog from other cell sources, including mammalian (specifically human).

Example 6 describes yeast RNA blots hybridized with a CN1c probe. Exemplary data are shown in Figure 11. A single message of approximately 2.9 kb is detected. The data indicate that CNI is an expressed gene encoding a 2.9 kb message in yeast.

Example 8 details the construction of cni null mutants. The null mutants are employed to assess if *CNI* is required for viability in yeast, and to test hygromycin B sensitivity. The experiments indicate that CNI is not essential for viability, since CNI deletion mutant strains can survive, but that CNI deletions render a host more resistant to hygromycin B. The effect is particularly pronounced in both MCY300-1 (*cna1<sup>-</sup>cna2<sup>-</sup>*) and DD12 (*cnb1<sup>-</sup>*), suggesting that CNI functions as a suppressor of CNI mutant's sensitivity to hygromycin B.

It will be understood that all of the above methods and experimental manipulations are amenable to being done with interacting polypeptides from organisms other than yeast. In particular, calcineurin subunits, CNI polypeptides, immunophilins and the like may be of mammalian origin, *e.g.*, human origin.

## VII. UTILITY

Methods and compositions of the present invention may be applied in a number of different ways. Following the guidance presented herein, one of skill in the art may isolate nucleic acids encoding additional CNI polypeptides, for example, a human CNI polypeptide.

In one approach, a yeast strain carrying a mutation of the *CNI* gene, *e.g.*, a deletion, is used to clone heterologous sequences (*e.g.*, human sequences) by complementation. A library of genomic DNA or, preferably, cDNA from an organism (*e.g.*, human) and tissue (*e.g.*, lymphocyte cells) of choice is cloned into a vector that can be maintained in yeast. Preferably, the vector contains a yeast promoter effective to express the heterologous sequences in yeast cells. Several heterologous libraries suitable for expression in *Saccharomyces*

*cerevisiae* containing DNA from *S. pombe* (Beach, *et al.*) and *Drosophila* have been constructed.

The library is transformed into a suitable yeast strain carrying a *cni* mutation, and transformants are selected using a suitable complementation assay. For example, transformants  
5 may be screened for increased hygromycin sensitivity, as experiments described herein indicate that *cni* deletion mutants possess a decreased sensitivity to hygromycin B (Example 8). The screen may be made more effective by using a yeast strain that is hypersensitive to hygromycin B, such as a strain deficient for a subunit of calcineurin (Example 8).

Alternatively, human CNI DNA sequences may be isolated by directly screening a  
10 library, *e.g.*, a lymphocyte cDNA library, for clones hybridizing with a yeast CNI nucleic acid probe. The generation of an exemplary yeast CNI nucleic acid probe is described in Example 1.

In another approach, particularly advantageous for isolating sequences expressed at low levels, a CNI nucleic acid probe may be used to screen a genomic library, *e.g.*, a human  
15 genomic library, to isolate a sequence that may be used to design probes or primers that may match the target sequence better than the yeast sequence. Such primers may be used with, for example, PCR, to isolate longer fragments from a tissue-specific library.

In yet another approach, an antibody generated against CNI polypeptide is used to immunoprecipitate a CNI polypeptide from an organism and/or tissue of choice. The protein  
20 may then be micro-sequenced, and the sequence utilized to design degenerate primers useful for isolating a cDNA.

CNI polypeptides of the present invention, particularly CNI fragments that retain a desired binding activity, may be used as lead compounds useful for the development of small molecules having cellular functions similar to those of the CNI-polypeptides, that is, molecules  
25 effective to enhance immunosuppressive effects of calcineurin-targeted immunosuppressants by potentiating an interaction of an immunophilin with calcineurin.

CNI-polypeptides of the present invention may also be employed in a method of increasing sensitivity of cells to calcineurin-affecting immunosuppressant drugs. In this method, a CNI-polypeptide is introduced into the cell typically prior to or at the same time as  
30 contacting the cell with an immunosuppressant drug, such as FK506. The polypeptide may be delivered by any suitable means effective to deliver polypeptides to selected cells.

Alternatively, nucleic acids encoding CNI polypeptides may be used in appropriate expression vectors as a genetic therapy tool to potentiate the immunosuppressive effects of

calcineurin-targeting immunosuppressant drugs. The vectors may be targeted to selected cells, such as T-cells, to increase their sensitivity to a given systemic dose of an immunosuppressant.

Another utility of the present invention includes methods of screening for substances that up-regulate expression of CNI polypeptides, *i.e.*, substances that affect transcription. Such substances are useful for sensitizing cells to immunosuppressant drugs. In this method, the CNI promoter can be attached to a gene that functions as a selectable marker (for use in genetic selections to screen test substances) or to a reporter gene (for use in evaluating the effect on CNI transcription by test substances).

In another aspect of the present invention, the CNI-polypeptides, for example, mammalian homologue polypeptides of CNI, have potential use as therapeutic agents for both human and veterinary use. For example, CNI-polypeptides may be used in a method of enhancing immunosuppression in a test subject. In this method, the CNI-polypeptide is administered to the subject in a pharmaceutically-acceptable formulation and at a concentration effective to potentiate the interaction of an immunosuppressant/immunophilin complex with a subunit of calcineurin. The method may also include contacting the CNI-polypeptide with a cell under conditions effective to permit uptake of the protein into the cell in order to increase sensitivity of the cell to immunosuppressants. A CNI polypeptide used in such methods may be modified to be more suitable for administration or to be more effective in a cell. For example, a CNI polypeptide may be modified to eliminate PEST motifs, which are typically found in proteins with short half-lives, to extend the effective lifetime of the polypeptide in the target cell.

The following examples illustrate, but in no way are intended to limit the present invention.

25

#### MATERIALS AND METHODS

Unless indicated otherwise, chemicals and reagents were obtained from Sigma Chemical Company (St. Louis, MO) or Mallinckrodt Specialty Chemicals (Chesterfield, MO), restriction endonucleases were obtained from New England Biolabs (Beverly, MA), and other modifying enzymes and biochemicals were obtained from Pharmacia Biotech (Piscataway, NJ) or Boehringer Mannheim (Indianapolis, IN). FK506 was obtained from Fujisawa USA, Inc. (Deerfield, IL), cyclosporin A was obtained from Sandoz (Basel, Switzerland), and rapamycin was obtained from Wyeth-Ayerst (Princeton, NJ). Materials for media for yeast growth and culture were obtained from DIFCO (Detroit, MI). Unless otherwise indicated, manipulations



of yeast, bacteria, nucleic acids, proteins and antibodies were performed using standard methods and protocols (*e.g.*, Guthrie, *et al.*, Sambrook, *et al.*, Ausubel, *et al.*, Harlow, *et al.*, and Rose, *et al.*).

#### 5           A.       Buffers

Z buffer: 60 mM Na<sub>2</sub>HPO<sub>4</sub>-7H<sub>2</sub>O, 40 mM NaH<sub>2</sub>PO<sub>4</sub>-H<sub>2</sub>O, 10 mM KCl, 1 mM MgSO<sub>4</sub>-7H<sub>2</sub>O and 50 mM β-mercaptoethanol (pH 7.0).

#### B.       Plasmids, Libraries and Yeast Strains

10           Plasmids pGBT9 (GBT), carrying GAL4 DNA-binding domain (amino acid residues 1-147; G4BD) and TRP1, and pGAD (GAD), carrying GAL4 activation domain (amino acid residues 768-881; G4AD) and LEU2; three pGAD libraries carrying fusions between G4AD and yeast genomic *Sau3AI* partial-digest fragments in each frame; and the yeast *GAL1-lacZ* reporter strain SFY526 (Y526; *MATa ura3-52 ade2-101 lys2-801 his3-200 trp1-901 leu2-3,112*  
15 *can1 gal4-542 gal80-538 URA3::GAL1-lacZ*) were obtained from Stanley Fields (State University of New York at Stony Brook, Stony Brook, NY; Chien, *et al.*, Bartel, *et al.*). The libraries were constructed with linkers between the GAL4 activation domain and the *Sau3AI* fragments. The sequences of the linkers were 5'-ATCG-3' for the first library, 5'-ATCCG-3' for the second library, and 5'-ATCCCG-3' for the third library. In this way, the yeast  
20 genomic *Sau3AI* fragments were cloned in all three reading frames relative to G4AD.

Plasmids pAS2 (AS) carrying G4BD and TRP1, and pAS-lamin (AS-lamin) containing a sequence encoding a G4BD-lamin C fusion; and yeast reporter strains Y190 (*MATa ura3-52 ade2-101 his3-Δ200 trp1-901 leu2-3,112 cyh2Δ, gal4Δ gal80Δ URA3::GAL-lacZ LYS2::GAL-HIS3*), a derivative of Y153 carrying dual indicator genes (GAL-lacZ and GAL-HIS3), and Y187 (*MATa ura3-52 ade2-101 lys2-801 his3-200 trp1-901 leu2-3,112 gal4Δ gal80Δ URA3::GAL-lacZ*) carrying *GAL-lacZ* reporter were obtained from Stephen Elledge (Baylor College of Medicine, Houston, TX; Durfee, *et al.*). Yeast strain Y153b1 (*cnb1::ADE2*) was derived from Y153.

*E coli* strain JBe181 (*leuB600 trpC9830*) was obtained from Ira Herskowitz (University  
30 of California at San Francisco, San Francisco, CA). Protease-deficient yeast strain BJ2407 (Guthrie, *et al.*) was obtained from the Yeast Genetic Center (University of California at Berkeley, Berkeley, CA).

### C. GAL4-Calcineurin Fusions

GAL4-calcineurin (GAL4-CN) fusions, GBT-A1 (G4BD-CNA1), GBT-A2 (G4BD-CNA2), GBT-B1 (G4BD-CNB1), GAD-A1 (G4AD-CNA1), GAD-A2 (G4AD-CNA2), and GAD-B1 (G4AD-CNB1) were constructed as follows. Plasmids containing inserts encoding  
5 CN subunits CNA1 (SEQ ID NO:9; Cyert, *et al.*, 1991), CNA2 (SEQ ID NO:11; Cyert, *et al.*, 1991) and CNB1 (SEQ ID NO:13; Cyert, *et al.*, 1992) were subjected to site-directed mutagenesis (Kunkle) to introduce a *Bam*HI site just upstream of each subunit's initiation codon in the second reading frame. DNA prepared from the mutated plasmids was digested with  
10 *Bam*HI and *Xho*I, and the resulting *Bam*HI-*Xho*I fragments, each containing a full-length coding sequence, were cloned into GBT or GAD that had been cut with *Bam*HI and *Sal* I. The resulting plasmids encoded in-frame fusions of the CN subunits with G4BD or G4AD.

Plasmids encoding CNA protein variants with truncated C-termini (GBT-A1ΔC, GBT-A2ΔC) were constructed by introducing stop codons after amino acid residues 509 (CNA1) and 502 (CNA2). The 44-residue deletion in GBT-A1ΔC removed the autoinhibitory domain of  
15 CNA1, while the 102-residue deletion in GBT-A2ΔC removed both the autoinhibitory and the calmodulin-binding domains of CNA2 (Cyert, *et al.*, 1991).

Plasmid GBT-FKBP, containing an FK506 binding protein (FKBP) gene fused to the GAL4 binding domain, was constructed by introducing a *Bgl*II site upstream of the initiation codon and a *Bam*HI site downstream of the stop codon of FKBP12 (Heitman, *et al.*) and  
20 ligating the *Bgl*II-*Bam*HI fragment into GBT cut with *Bam*HI.

Plasmid B1/YEp352 was constructed to contain the full coding sequence of CNB1 (SEQ ID NO:13, Cyert, *et al.*, 1992) as a 1.4 kb *Bam*HI-*Eco*RI fragment encompassing the sequence presented as SEQ ID NO:13 (812 bp; contains the coding sequence), in the multicopy plasmid YEp352(HIS), which is derived from YEp352 (URA) (Hill, *et al.*).

25 Plasmid CNI/YEp352(HIS) (also referred to as CNIH) was constructed by ligating a 3.16 kb *Mun*I-*Eco*RV fragment, containing the full coding sequence of CNI, from plasmid CNI7.1 (construction described below) into YEp352(HIS) cut with *Eco*RI and *Sma*I. Plasmids CNI/YEp352(TRP) (also referred to as CNIT) and CNI/YEp352(URA) (also referred to as CNIU) were similarly constructed using the 3.16 kb fragment and YEp352(TRP) or  
30 YEp352(URA), respectively (Hill, *et al.*).

Plasmids A1/YEp351 and A2/YEp352 were constructed to contain the full coding sequences of CNA1 (SEQ ID NO:9, Cyert, *et al.*, 1991) in YEp351 (Hill, *et al.*) and CNA2 (SEQ ID NO:11, Cyert, *et al.*, 1991) in YEp351 and YEp352, respectively. A1/YEp351 was constructed by ligating a 2.9 kb *Sac*I-*Hind*III fragment from clone CNA1 (Cyert, *et al.*, 1991)

into YEp351(HIS) cut with *SacI* and *HindIII*. A2/YEp352 was similarly constructed by ligating a 3 kb *SpeI-HindIII* fragment from clone CNA2 (Cyert, *et al.*, 1991) into YEp352(HIS) cut with *XbaI* and *HindIII*.

5 All GAL4-CN fusions were verified by DNA sequencing (Sanger, *et al.*) using "SEQUENASE 2.0" sequencing kits (United States Biochemical, Cleveland, OH), and were subjected to the following tests. The functionality of the fusion proteins was assayed by determining whether they could complement the appropriate *cn*<sup>-</sup> mutant phenotypes, using assays to measure the sensitivity to pheromone and Mn<sup>2+</sup> (Reneke, *et al.*, Cyert, *et al.*, 1991). All of the GAL4-CN fusions were functional in this assay.

10 The fusion proteins were also tested for their ability to activate the reporter gene in the absence of the complementary GAL-4 domain fusion (*i.e.*, in the presence of the complementary GAL4 domain not fused to a second protein, for example, G4BD-A1 vs G4AD) using the two-hybrid interaction assay described below. Only GBT-B1 and GAD-A1 were able to activate the reporter gene at low levels without the complimentary GAL-4 domain fusion --  
15 assays with the other fusion proteins in the absence of the complimentary GAL-4 domain fusion showed no detectable levels of expression.

The two-hybrid interaction assay was also used to test the ability of the fusions to interact specifically with another fusion containing complimentary GAL4 and CN domains (*e.g.*, G4BD-A1 interacting with G4AD-B1). All CN hybrids were able to react specifically  
20 and result in an activation of the reporter gene that was clearly detectable above background. The high specificity witnessed in these experiments indicates that the GAL4 two-hybrid system can reliably be used to assay interactions between CN and other proteins.

#### D. Yeast GAL4 Two-Hybrid System for Detecting Protein-Protein Interaction

25 In the library screen, described in more detail in Example 1A, the yeast strain Y190, harboring the hybrid plasmid carrying the GAL4 binding domain fused to the A1 subunit of calcineurin (G4BD-CNA1), was transformed with fusion libraries carrying yeast genomic DNA *Sau3AI* fragments fused to the GAL4 activation domain. Transformants that were able to express the reporter genes, *i.e.*, able to grow on -His + 3-AT and to score blue in  $\beta$ -gal assay,  
30 were selected as candidate positives. These candidate positives potentially contain library DNA fragments encoding proteins that physically interact with CNA1.

In another application described herein, the two-hybrid system was used to test for interactions between CNA (fused to one of the GAL4 domains) and CNB1 (fused to the other GAL4 domain), and between CNA and FKBP. Additional experiments tested a clone, CN1c,

isolated using the library screen, against a series of proteins fused to the complementary GAL4 domain under various conditions to test whether CN1c interacts with CNA subunits, and if so, how the interactions are affected by various conditions.

5           E.     Color Development ( $\beta$ -gal) Assay

Yeast reporters harboring both G4BD and G4AD fusions (and a third non-fusion plasmid in some cases) were monitored for  $\beta$ -gal activity as follows. Purified yeast transformants were patched onto selective plates with or without other test reagents. After growing 3 days at 30°C, colonies were lifted onto nitrocellulose filters, permeabilized in liquid  
10   nitrogen as above, placed on Whatman No. 1 paper in petri dishes containing 0.1% X-Gal in Z buffer (see above), and incubated at 30°C for 12 hours. Blue color begins to appear in positive colonies between about one half and ten hours into the incubation period.

Exemplary images obtained using the color development assay are presented in Figures 2A, 3A, 4A, 4C, 5A, 5C, 6A, 6C, 6F, 7A, 7C, 7E, 7G, 8A, 9A and 9C.

15

F.     Growth Assay

A growth assay, applicable to yeast strains Y190 and Y153b1 which carry both *GAL-HIS3* and *GAL-lacZ* reporters, was sometimes used as a complement to the color assay described above. Yeast transformants were streaked onto selective plates containing 40-50 mM  
20   3-AT and no Histidine, and incubated at 30°C for 3-7 days. Growth (corresponding to the level of *HIS3* expression) was monitored as an indicator of the interaction between fusion proteins. In cases where both assays were used, the amount of cell growth typically correlated well with the color intensity in the  $\beta$ -gal assay.

25           G.     Yeast Growth, Drug Treatment

Yeast were typically grown in YPD (rich non-selective) or synthetic complete (SC) medium with selected component drop-outs, depending on the plasmid introduced, following standard procedures (Sherman, *et al.*, Ausubel, *et al.*).

Experiments utilizing treatment with drugs or additives were performed by including  
30   the drug or additive in the medium. For plating, the agar was autoclaved, allowed to cool to 50°C, and the drug or additive was added before pouring the plates. Unless otherwise indicated, drugs and additives were added to result in the following final medium concentrations: FK506: 1  $\mu$ g/ml, cyclosporin A: 10  $\mu$ g/ml, rapamycin: 10 ng/ml, and hygromycin B: 40  $\mu$ g/ml.

## H. Antibodies

Polyclonal and monoclonal antibodies, for use in the present invention, can be prepared by standard methods (Harlow, *et al.*) utilizing the CNI polypeptides of the present invention, for example, a substantially purified CNI/ $\beta$ -galactosidase fusion protein (Example 9).  
5 Antibodies can also be generated by recombinant techniques (Cabilly, *et al.*; Better, *et al.*; Skerra, *et al.*). In addition to whole antibody molecules, antibody fragments retaining the immunological specificity of the whole antibody may also be used in the practice of the present invention (*e.g.*, Fab and F(ab')<sub>2</sub> fragments of IgG (Pierce Chemical, Rockford, IL)). The antibodies can be purified by standard methods to provide antibody preparations which are  
10 substantially free of serum proteins that may affect reactivity (*e.g.*, affinity purification (Harlow *et al.*)).

## EXAMPLE 1

### Isolation of CN1c

#### 15 A. Library Screening

Yeast strain Y190 was transformed with pGBT-CNA1 *TRP1* (GBT-A1) hybrid plasmid using the transformation protocol described by Schiestl, *et al.* Transformants were selected, colony purified, and a single transformant was selected to make (Y190 GBT-A1)-competent cells, following the procedure described in Guthrie, *et al.*.

20 The three pGAD yeast fusion libraries described above, carrying fusions between G4AD and yeast genomic DNA *Sau3A*I fragments in each reading frame, were then used to transform (Schiestl, *et al.*) the Y190 GBT-A1-containing cells. Transformants were plated onto SC-Trp-Leu-His plates containing 40 mM 3-aminotriazole (3-AT; Sigma Chemical Co., St. Louis, MO) and incubated at 30°C for 6 days to screen for HIS<sup>+</sup> colonies (Durfee, *et al.*).

25 His<sup>+</sup> colonies were replica plated onto nitrocellulose filters (Schleicher & Schuell, Keene, NH), frozen in liquid nitrogen for approximately 30 seconds, and incubated at 30°C for 12 hours with Z buffer (see above) containing the chromogenic substrate X-Gal (0.1%) to assay  $\beta$ -gal activity (Breden, *et al.*).

Candidate positive (blue) colonies were re-streaked for single colonies. Single colonies  
30 were purified and retested using the above protocol. Colonies which reproducibly tested positive were screened using PCR with primers directed against the internal portion of GAL-4 (*i.e.* the portion between the DNA binding domain and the activation domain). The sequences of the primers, G4-PCR-A and G4-PCR-B, are given as SEQ ID NO:22 and SEQ ID NO:23,

respectively. Colonies yielding a PCR product were identified as containing intact GAL4, and were eliminated.

The GBT-A1 *TRP*<sup>+</sup> plasmid was eliminated by growing in Trp<sup>+</sup> liquid media for 2-3 days, plating on -Leu media and then replica-plating on -Leu and -Trp plates to identify and  
5 eliminate colonies that had lost the GBT-A1 plasmid, yet still gave a positive signal.

Plasmid DNA was extracted from the remaining Leu<sup>+</sup> candidates. The plasmid DNA was transformed into *E coli* JBe181 and plated on -Leu media to select for library plasmids. The library plasmids isolated by this method were introduced back to the yeast reporter strains either alone or with test G4BD fusions: GBT, GBT-A1, and AS-lamin.

10 A parallel specificity assay was conducted by mating. Candidate strains, as described above, were 3-AT growth positive and X-gal positive when both the library and GBT-A1 plasmids were present. After elimination of the GBT-A1 plasmid from these strains, strains that were Leu<sup>+</sup> Trp<sup>-</sup> 3-AT growth<sup>-</sup> and  $\beta$ -gal<sup>-</sup> were mated to the following strains: Y187 (*MAT $\alpha$* ) carrying GBT, GBT-A1, or AS-lamin, and the diploids were assayed.

15 Among the 3-AT positive,  $\beta$ -gal positive candidates identified by the secondary screening method just described, one clone (III-21S, later termed GAD-CN1c) was specifically positive in conjunction with GBT-A1 in both the transformation assay and the mating assay.

#### B. Sequence of CN1c

20 Clone III-21S was sequenced as above. The sequence is presented herein as SEQ ID NO:1, and a schematic representation of the clone is shown in Figure 1A. The *Sau3AI* library insert encodes 306 amino acids followed by a stop codon in frame with the coding sequence of GAL4, but does not contain an in-frame ATG start site upstream of the stop codon. This is consistent with the fragment encoding a c-terminal portion of a complete gene product.  
25 Accordingly, the clone was termed CN1c, with the lowercase "c" representing "c-terminal".

The stippled portion between GAL-4AD and CN1c in Figure 1A represents the linker discussed in Materials and Methods, above. Also indicated in the Figure are the approximate locations of in-frame start (ATG) and stop codons, and *Sau3AI* restriction sites.

#### 30 C. Isolation of a Full Length Clone

A <sup>32</sup>P-labeled CN1c probe was generated from the 1.22 kb CN1c insert of clone III-21S by polymerase chain reaction (PCR) using primers represented as SEQ ID NO:7 and SEQ ID NO:8. The probe was used to map the gene to the right arm of chromosome 11 by hybridization screening (Sambrook, *et al.*) a panel of  $\lambda$  clones (American Type Culture

Collection (ATCC), Rockville, MD) spanning the entire yeast genome. Two clones, 70500 and 70590, gave positive hybridization signals. A phage lysate of clone 70500 in  $\lambda$  MG3 was obtained from the ATCC, was amplified, purified, restriction-mapped and used as a DNA source for subsequent cloning experiments.

- 5 The phage DNA was digested with *SacI*, yielding a 7.1 kb fragment containing the entire CNI gene. This fragment was cloned into "BLUESCRIPT SK" (Stratagene, La Jolla, CA) cut with *SacI*, yielding plasmid CNI7.1. Plasmid CNI7.1 was digested with *MunI* and *EcoRV*, releasing a 3.16 kb fragment containing the entire coding sequence of CNI. The 3.16 kb fragment was then cloned into each of YEp352(HIS), YEp352(TRP), YEp352(URA), and
- 10 "BLUESCRIPT SK", each cut with *EcoRI* and *SmaI*, yielding plasmids CNIH, CNIT, CNIU and CNI3.2, respectively. The sequence of the 3.16 kb *MunI/EcoRV* fragment is encompassed by the 3.5 kb sequence presented as SEQ ID NO:4. The *MunI* site is at nucleotide 100 of SEQ ID NO:4, and the *EcoRV* site is at nucleotide 3263 of SEQ ID NO:4.

- A schematic diagram of the sequence presented as SEQ ID NO:4 is shown in Figure
- 15 1B. This sequence contains the 3.16 kb *MunI/EcoRV* fragment used in many of the experiments described herein (depicted in Figure 1B as the portion between the *MunI* and *EcoRV* sites), which contains the entire 2.75 kb coding sequence of CNI (SEQ ID NO:6; graphically indicated in Figure 1B by the locations of the "ATG" and "Stop" codons).

- Figure 13 also shows the location of certain features of the sequence. For example,
- 20 "PEST" motifs (Rogers, *et al.*, Dice) are indicated by bars over the corresponding sequence.

A search of known DNA and protein sequences turned up no obvious matches or homologies to genes in other organisms. Accordingly, CNI may represent a new type of calcineurin-binding protein.

25

## EXAMPLE 2

### Binding of CNIC to Calcineurin

Y190 yeast carrying the plasmids indicated below were assayed for  $\beta$ -gal activity by color development assay described above to determine the specificity of binding of CNIC to subunits of calcineurin.

- 30 Exemplary data, in the form of images of filters having yeast colony replicas that had undergone the  $\beta$ -gal color development assay are shown in Figure 2A. The legend for Fig. 2A is shown in Figure 2B. Numbers in the legend refer to locations of yeast colonies expressing particular combinations of plasmid constructs. The constructs are as follows: 20:GBT-A1 and

GAD-B1, 21:GBT-A1 and GAD-CN1c, 22:GBT-A1 and GAD-CN1c, 23:GBT-A1 and GAD-CN1c 24:GBT-A2 and GAD-CN1c 25:AS-lamin and GAD-CN1c 26:GBT and GAD-CN1c.

Yeast colonies used in the assay were derived by several different methods. Those at location 22 were purified colonies from the original library screen, those at 21 were colonies  
5 transformed with mini-prep DNA of the isolated GAD-CN1c plasmid, and the remaining colonies (23, 24, 25 and 26) were transformed with maxi-prep (Qiagen, Chatsworth, CA) DNA of GAD-CN1c.

A comparison of the intensities of the blue  $\beta$ -gal reaction product indicates that CN1c interacted strongly with CNA1 regardless of the source of the CN1c plasmid DNA (20, 21, 22  
10 and 23), and somewhat less strongly with CNA2 (24). Neither cells containing AS-lamin with GAD-CN1c (25), nor cells containing only GBT with GAD-CN1c (26) showed a detectable signal above background. Two subunits of calcineurin (CNA1, CNB1) known to interact were used as a positive control for the assay (20).

In summary, the data above show that CN1c interacted specifically with CNA1 and  
15 CNA2, but not with G4BD or lamin C.

A similar set of experiments was conducted using constitutively-active CNA subunits, as well as calcineurin subunit CNB1. As described in Materials and Methods, above, CNA1 $\Delta$ C and CNA2 $\Delta$ C were each missing a C-terminal portion of the protein containing an autoinhibitory domain. Exemplary results from these experiments are shown in Figure 3A.  
20 The legend for Fig. 3A is shown in Figure 3B. Locations of yeast colonies expressing specific constructs are as follows: 27:GBT and GAD-CN1c, 28:GBT-A1 $\Delta$ C and GAD-CN1c, 29:GBT-A2 $\Delta$ C and GAD-CN1c, 30:GBT-A1 $\Delta$ C and GAD, 31:GBT-A2 $\Delta$ C and GAD, 32:GBT-B1 and GAD-CN1c, 33:GBT-B1 and GAD, 34:GBT-A1 $\Delta$ C and GAD-B1, and 35:GBT-A2 $\Delta$ C and GAD-B1.

25 The data show that GBT-A1 $\Delta$ C and GAD-CN1c (28) gave a definite positive signal, while GBT-A2 $\Delta$ C and GAD-CN1c (29) was weaker, though still detectable above its background (*i.e.* GBT-A2 $\Delta$ C and GAD; 31). The signal from GBT-B1 and GAD-CN1c (32) was not detectable above vector background (GBT-B1 and GAD; 33). Positive controls GBT-A1 $\Delta$ C and GAD-B1 (34) and GBT-A2 $\Delta$ C and GAD-B1 (35) gave strong signals.

30 These data show that CN1c interacted specifically with CNA1 $\Delta$ C and CNA2 $\Delta$ C, but not with CNB1.



**EXAMPLE 3****Effects of Immunosuppressant Drugs on Binding of CN1c to Calcineurin in B1<sup>+</sup>, B1****Deletion and B1 Overproducing Yeast Strains**

Three yeast strains carrying the plasmids indicated below were assayed for  $\beta$ -gal activity as above to determine if the immunosuppressant drugs FK506, cyclosporin A (CsA) and rapamycin affect the binding of CN1c to subunits of calcineurin. The experiments were performed in yeast strains wild-type for the CNB1 subunit, null for the CNB1 subunit, and in yeast transformed with a high efficiency expression vector containing DNA encoding the CNB1 subunit.

Exemplary data, in the form of filter images produced as above are shown in Figures 4A, 4C, 5A and 5C. Plates used to make the filters shown in Figs. 4A and 4C were replicas from one master plate, while plates used to make the filters shown in Figs. 5A and 5C were replicas from another plate. The plates used to generate filters shown in Figs. 4A and 5A were without FK506, while the plates used to generate filters shown in Figs. 4C and 5C contained 1  $\mu$ g/ml FK506.

The legends for Figs. 4A and 4C are shown in Figures 4B and 4D, respectively. Since the imaged filters in Figs. 4A and 4C were from replica plates, corresponding locations on each filter contain material from the same yeast colonies. Accordingly, the locations are referred to by the same "base" numbers in the legends. To facilitate reference to a specific location on a specific filter, the base numbers are followed by a lowercase letter that is different for each of the individual filters. For example, in the present figure, "a" follows the base numbers to identify locations on the filter shown in Fig. 4A, while a "b" follows the base numbers to identify locations on the plate in Fig. 4C. This labeling scheme is used in other experiments detailed herein where multiple filter lifts are shown.

The interactions of various combinations of proteins expressed by constructs indicated below was studied in three yeast strains. Strain Y153b<sup>+</sup>, at 36-40, is null for the CNB1 subunit of calcineurin. Strains Y190 (41-46) and Y526 (47-51) are wild-type for CNA1, CNA2 and CNB1.

Hybrid proteins expressed by colonies at specific locations are as follows: 36:GBT-A1 and GAD-CN1c, 37:GBT-A2 and GAD-CN1c, 38:GBT-A1 $\Delta$ C and GAD-CN1c, 39:GBT and GAD-CN1c, 40:GBT-A2 $\Delta$ C and GAD-CN1c, 41:GBT-A1 and GAD-CN1c, 42:GBT and GAD-CN1c, 43:GBT-A2 and GAD-CN1c, 44:GBT-A1 $\Delta$ C and GAD-CN1c, 45:GBT-A1 and GAD-B1, 46:GBT-A2 $\Delta$ C and GAD-CN1c, 47:GBT-A1 and GAD-CN1c, 48:GBT and GAD-CN1c,

49:GBT-A2 and GAD-CN1c, 50:GBT-A1 $\Delta$ C and GAD-CN1c, and 51:GBT-A2 $\Delta$ C and GAD-CN1c.

Yeast strain Y526 was used for all experiments shown in Figs. 5A, 5B, 5C and 5D. The expression vector B1/YEp352(HIS) was not used in strains Y190 or Y153b1 because they  
5 are HIS<sup>+</sup> in the absence of 3-AT.

The base numbers in Figures 5B and 5D correspond to locations of colonies expressing the following constructs: 52:GBT-A1, GAD-CN1c and YEp352, 53:GBT-A1, GAD-CN1c and B1/YEp352, 54:GBT-A2, GAD-CN1c and YEp352, 55:GBT-A2, GAD-CN1c and B1/YEp352, 56:GBT, GAD-CN1c and B1/YEp352, 57:GBT-A1 $\Delta$ C, GAD-CN1c and B1/YEp352, and  
10 58:GBT-A2 $\Delta$ C, GAD-CN1c and B1/YEp352.

A comparison of data shown in Fig. 4A (no added drugs) shows the effect of deleting the endogenous host CNB1 gene on interactions between CN1c and calcineurin subunits CNA1, CNA2, CNA1 $\Delta$ C and CNA2 $\Delta$ C. Note that interactions in panels 36a-40a (CNB1 null strain) were all stronger (with the exception of the negative control in 39) than interactions in  
15 corresponding panels 41a-51a (strains wild-type for CNB1). This result indicates that interaction between CN1c and CNA subunits were enhanced by the deletion of the CNB1 subunit.

Comparison of corresponding panels in Figs. 4A and 4C shows the effects of FK506 on CN1c-CNA/CNA $\Delta$ C interactions. The drug enhanced interactions under all except control  
20 (39, 42 and 48) conditions. The effect was most striking in yeast strains wild-type for the CNB1 subunit (*e.g.*, compare 50a with 50b, and 51a with 51b).

The drug also markedly enhanced CN1c-CNA/CNA $\Delta$ C interactions under conditions where the CNB1 subunit was overexpressed. Figure 5A shows the effect of overexpressing CNB1 on CN1c-CNA/CNA $\Delta$ C interactions in the absence of drug. Colonies expressing  
25 B1/YEp352 (53a, 55a-58a) had reduced signal as compared with controls expressing only YEp352 (52a, 54a). Inclusion of FK506 in the plating medium (Fig. 5C), however, enhanced interactions in all colonies, except the negative controls (56).

Taken together, the above data demonstrate that the interaction of CN1c with CNA and CNA $\Delta$ C was markedly enhanced by FK506. The interaction was also enhanced by deletion  
30 of CNB1 and diminished by overexpression of CNB1, and the inhibitory effect of CNB1 overproduction was overcome by the stimulatory effect of FK506.

In light of the effects of FK506 on CN1c-CNA/CNA $\Delta$ C interactions, two other immunosuppressants, cyclosporin A and rapamycin, were examined in similar experiments. The results of these experiments are shown in Figures 6A-6F and 7A-7H. Filters shown in

Figs. 6A-6F were from replica plates, as were those in Figs. 7A-7H. Colonies shown in Figs. 6A and 7A were plated without drugs; those in Figs. 6C and 7C were plated with FK506 (1  $\mu$ g/ml), those in Figs. 6E and 7E with CsA (10  $\mu$ g/ml), and those in Fig. 7G with rapamycin (10 ng/ml). Yeast strains used were as follows: In Figs. 6A-6F, panels 59-63 were Y153b1, 64-69 were Y190, and 70-74 were Y526. In Figs. 7A-7H, panels 77-83 were Y526, and panels 75 and 76 were Y190.

The base numbers in Figures 6B, 6D and 6F correspond to locations of colonies expressing the following constructs: 59:GBT-A1 and GAD-CNIc, 60:GBT-A2 and GAD-CNIc, 61:GBT-A1 $\Delta$ C and GAD-CNIc, 62:GBT and GAD-CNIc, 63:GBT-A2 $\Delta$ C and GAD-CNIc, 64:GBT-A1 and GAD-CNIc, 65:GBT and GAD-CNIc, 66:GBT-A2 and GAD-CNIc, 67:GBT-A1 $\Delta$ C and GAD-CNIc, 68:GBT-A1 and GAD-B1, 69:GBT-A2 $\Delta$ C and GAD-CNIc, 70:GBT-A1 and GAD-CNIc, 71:GBT and GAD-CNIc, 72:GBT-A2 and GAD-CNIc, 73:GBT-A1 $\Delta$ C and GAD-CNIc, and 74:GBT-A2 $\Delta$ C and GAD-CNIc.

The base numbers in Figures 7B, 7D, 7F and 7H correspond to locations of colonies expressing the following constructs: 75:GBT-FKBP and GAD, 76:GBT-FKBP and GAD-CNIc, 77:GBT-A1, GAD-CNIc and YEp352, 78:GBT-A1, GAD-CNIc and B1/YEp352, 79:GBT-A2, GAD-CNIc and YEp352, 80:GBT-A2, GAD-CNIc and B1/YEp352, 81:GBT, GAD-CNIc and B1/YEp352, 82:GBT-A1 $\Delta$ C, GAD-CNIc and B1/YEp352, and 83:GBT-A2 $\Delta$ C, GAD-CNIc and B1/YEp352.

The data presented in Figures 6A and 6C are essentially equivalent to those presented in Figures 4A and 4C, respectively. The constructs and yeast strains at corresponding locations were the same. As expected, the  $\beta$ -gal signal was also essentially equivalent between the two sets. Data shown in Figure 6E demonstrate that like FK506, the immunosuppressant cyclosporin A was also effective in enhancing interaction of CNIc with CNA and CNA $\Delta$ C. Both FK506 and cyclosporin A are known to exert their immunosuppressive effects through inhibition of calcineurin activity (Cyert).

Similarly, data shown in Figures 7A and 7C are essentially equivalent to those in Figures 5A and 5C, except that a top panel has been added in Figs. 7A-H. As above, the corresponding panels show the same constructs and yeast strains. The added panels (75 and 76) assessed the interaction of an FK506 binding protein (FKBP) with CNIc, and indicate that there were no detectable interactions between these proteins. Results in Fig. 7E demonstrate that cyclosporin A had a similar effect to FK506 in cells overexpressing CNB1 — that is, it enhanced the interactions between CNIc and CNA/CNA $\Delta$ C.

In contrast, data presented in Fig. 7G show that the immunosuppressant rapamycin, which is known not to target calcineurin, had no detectable effect on CN1c-CNA/CNAΔC interactions (compare Fig. 7G with Fig. 7A).

Taken together, the above data show that like FK506, cyclosporin A (CsA), but not rapamycin, also enhanced the interaction of CN1c with CNA and CNAΔC. CN1c didn't interact with FKBP with or without FK506.

#### EXAMPLE 4

##### Effects of CNI on FKBP/FK506 binding to Calcineurin

Y526 cells, carrying the plasmids indicated below, were grown in -Trp-Leu-His liquid media with or without FK506 (1 μg/ml) until OD<sub>600</sub> reached about 1.0. Approximately the same number of cells, calculated based on OD<sub>600</sub> and equivalent to 1 ml of an OD<sub>600</sub>=1 suspension, was harvested from each culture, washed once with ddH<sub>2</sub>O, centrifuged briefly, and the pellet was resuspended in 30 μl ddH<sub>2</sub>O and transferred onto a nitrocellulose filter. The filters were frozen in liquid nitrogen as described above, placed in a 8.5 cm petri dish containing a sheet of Whatman No. 1 paper (Whatman International LTD, Maidstone, UK) in 1.6 ml Z buffer containing 0.1% X-Gal, and incubated at 30°C for 8 hours.

Figure 8A presents exemplary data from studies to assess the effect of CNI overexpression on FK506-mediated FKBP interactions with CNA2. The legend for Fig. 8A is shown in Figure 8B. Locations of yeast colonies expressing specific constructs: 84:GBT-FKBP, GAD-A2 and YEp352, 85:GBT-FKBP, GAD-A2 and YEp352, 86:GBT-FKBP, GAD-A2 and CNI/YEp352, and 87:GBT-FKBP, GAD-A2 and CNI/YEp352. The cells at 85 and 87 were exposed to FK506, while those at 84 and 86 were not.

Data in Figure 8A demonstrate that, in the absence of FK506, FKBP and CNA2 showed no detectable interaction (84). In the presence of FK506, however, the proteins interacted (85), presumably because FK506 formed a complex with FKBP, which then bound CNA2 (Cyert).

Data in Figure 8A further show that, in the absence of FK506, CNI had no effect on the lack of interaction between FKBP and CNA2 (86). In the presence of FK506 (87), however, CNI potentiated, or enhanced the binding between FKBP and CNA2 (compare the intensity at 87 with that at 85). This effect suggests that CNI and similar compounds may be employed to increase the sensitivity of calcineurin to immunosuppressant drugs that act on it, and in this way, decrease the amount of the immunosuppressant required for a particular level of immunosuppression.

Experiments illustrated in Figures 9A and 9B demonstrate that CNI overproduction had little or no effect on the binding of CNA2 to CNB1, providing support for the specificity of the stimulatory effect that CNI overproduction had on the FK506-dependent binding of FKBP to calcineurin. The legends for Fig. 9A and 9B are shown in Figures 9B and 9D, respectively.

- 5 Locations of yeast colonies expressing the following constructs: 88:GBT-A2, GAD-B1 and YEp352, 89:GBT-A2, GAD-B1 and YEp352, 90:GBT-A2, GAD-B1 and CNI/YEp352, and 91:GBT-A2, GAD-B1 and CNI/YEp352. The colonies at 89 and 91 were exposed to FK506, while colonies at 88 and 90 were not.

- 10 Taken together, the above data show that overexpression of the full-length CNI clone markedly enhanced the FK506-dependent interaction of FKBP with CNA, although it didn't affect the interaction between CNA and CNB1.

#### EXAMPLE 5

##### Co-Immunoprecipitation of CN1c and CNA

- 15 Yeast BJ2407 harboring AS-CN1c, which carries an influenza hemagglutinin (HA) epitope tag (Wilson, *et al.*), and GAD-A2 (lanes 1, 3) or A2/YEp352 (lanes 2, 5), and strain MCY300-1 (*cna1<sup>-</sup>cna2<sup>-</sup>*; lane 4) were grown in selective media to  $OD_{600}=0.8$ . The cells were harvested, lysed, and immunoprecipitated in the presence of 25  $\mu$ g/ml FK506 with anti-HA monoclonal antibody (obtained from M. Kirschner, Harvard University, Boston, MA; Wilson, *et al.*), following protocols described in Harlow, *et al.* The cell extracts (lanes 3-5) and the  
20 immune complex (lanes 1, 2) were resolved by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE; Laemmli) followed by western blot with a rabbit anti-CNA2 polyclonal antibody generated using standard methods (Harlow, *et al.*). Bound anti-CNA2 antibody was visualized with the "ECL" kit (Amersham, Arlington Heights, IL) using goat anti-  
25 rabbit antibody. Molecular weight markers are indicated on the right in kD.

The results demonstrate that CN1c was capable of binding to CNA2 tightly enough for the complex to be co-immunoprecipitated. This independent, biochemical assay confirmed the results described above obtained using the two hybrid protein interaction assay -- that is, that CN1c physically interacted with and bound CNA subunits.

- 30 Cell extracts of BJ2407 harboring AS-CN1c, and GAD-A2 or A1/Yep351, and Y153b1 harboring AS-CN1c and GAD-A1 were subjected to SDS-PAGE followed by western blot with anti HA antibody. The results showed that CN1c was present at very low levels *in vivo*.

The results are consistent with the observations that a limited amount of CNA2 was precipitated by anti-HA antibody recognizing the CNIC fusions, and that CNI contains PEST-like motifs, a feature of proteins with a short half-life *in vivo* (Rogers, *et al.*).

5

#### EXAMPLE 6

##### Northern Blot of CNIC

Norther blots (*e.g.*, Sambrook, *et al.*) of yeast total RNA were hybridized with a CNIC probe. Exemplary data are shown in Figure 11. 20  $\mu$ g yeast RNA from YPH499 (lane 1) and MCY300-1 (lane 2) was resolved in a formaldehyde-agarose gel, transferred onto "HYBOND N+" membrane (Amersham, Arlington Heights, IL), and hybridized with  $5 \times 10^6$  cpm/ml probe of the CNIC insert (1.22kb). A single message of approximately 2.9 kb was detected in both strains at about the same level following an 18-hour exposure on XAR5 film (Eastman Kodak, Rochester, NY).

The data indicate that CNI was a physiologically expressed gene encoding a 2.9 kb message in yeast.

15

#### EXAMPLE 7

##### Chromosome Mapping of CNIC

A yeast chromosome blot obtained from the ATCC was hybridized with probe of the CNIC insert following the Southern hybridization procedure described in Sambrook, *et al.* A positive hybridization signal was obtained with two ATCC yeast genomic  $\lambda$  clones derived from chromosome 11. Clone 70500 had a relatively strong signal, while clone 70590 had a somewhat weaker one. A phage lysates of clone 70500 was ordered from the ATCC, amplified, purified, restriction-mapped, and used as a DNA source for cloning full length CNI (Example 1).

25

#### EXAMPLE 8

##### CNI null Mutants

###### 1. Construction of *cni* Null Mutation

A 5', 1.8 kb *Bgl*II-*Hind*III and a 3', 0.9 kb *Xba*I-*Bgl*II fragment of CNI were ligated into pRS305(LEU2) (Sikorski, *et al.*). The resultant plasmid had a deletion of a 2 kb *Hind*III-*Xba*I fragment from the coding sequence of CNI. This *cni::LEU2* mutant was introduced into the genomes of yeast haploid strains YPH499 (Sikorski, *et al.*), MCY300-1 (*cnal*<sup>-</sup> *cna2*<sup>-</sup>) and DD12 (*cnb1*<sup>-</sup>) (Cyert, *et al.*, 1991, Cyert, *et al.*, 1992) as well as two diploid strains.

30

Leucine prototrophs were isolated at high frequency from all strains, and hybridization analysis confirmed that the *cni::LEU2* allele had replaced the CNI gene. The experiments indicate that CNI is not essential for viability, since CNI deletion mutant strains (even *cni*<sup>-</sup> *cn*<sup>-</sup> double mutants) can survive.

5        *CNI* was deleted from three yeast strains: YPH499 (WT), MCY300-1 (*cna1*<sup>-</sup>*cna2*<sup>-</sup>), and DD12 (*cnb1*<sup>-</sup>), resulting in *cni*<sup>-</sup> strains LHy499, LHy300 and LHy12, respectively. Cells representing four colonies of each *cni* knockout strain and two colonies of each parent strain were grown in liquid YPD (Sherman, *et al.*) to saturation. Same numbers of cells from each culture were then plated onto YPD + Hygromycin B (40 µg/ml) and growth was monitored at  
10    30°C.

CNI deletions in each strain rendered that strain more resistant to hygromycin B. The effect was particularly pronounced in both MCY300-1 and DD12, suggesting that CNI functions as a suppressor of CN mutant's sensitivity to hygromycin B. The data indicate that deletion of *CNI* results in higher resistance to hygromycin B.

15

#### EXAMPLE 9

##### Isolation of CNI/β-Galactosidase Fusion Protein

A CNI coding sequence is cloned into the λ gt11 vector (Stratagene, La Jolla, CA). The coding frame is cloned in-frame to the β-galactosidase coding sequences present in λ gt11.  
20    Bacterial lysogens infected either with lambda phage gt11 or with gt11/CNI are incubated in 32°C until the culture reaches to an O.D. of 0.4. Then the culture is incubated in a 43°C water bath for 15 minutes to induce gt11 peptide synthesis, and further incubated at 37°C for 1 hour. Bacterial cells are pelleted and lysed in lysis buffer (10 mM Tris, pH 7.4, 2 % "TRITON X-100" and 1% aprotinin). Bacterial lysates are clarified by centrifugation (10K,  
25    for 10 minutes, Sorvall JA20 rotor) and the clarified lysates are incubated with Sepharose 4B beads conjugated with anti-β-galactosidase (Promega).

Binding and elution of β-galactosidase fusion proteins are performed according to the manufacturer's instruction. Typically binding of the proteins and washing of the column are done with lysis buffer. Bound proteins are eluted with 0.1 M carbonate/bicarbonate buffer,  
30    pH 10.

While the invention has been described with reference to specific methods and embodiments, it will be appreciated that various modifications and changes may be made without departing from the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: The Board of Trustees of the Leland Stanford Junior University
- (ii) TITLE OF INVENTION: Calcineurin Interacting Protein Compositions and Methods
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Dehlinger & Associates
  - (B) STREET: 350 Cambridge Avenue, Suite 250
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94306
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 23-OCT-1995
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/328,322
  - (B) FILING DATE: 24-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sholtz, Charles K.
  - (B) REGISTRATION NUMBER: P38,615
  - (C) REFERENCE/DOCKET NUMBER: 8600-0151.41
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 324-0880
  - (B) TELEFAX: (415) 324-0960

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL ISOLATE: Sau3AI fragment containing CN1c coding sequenc
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..918



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAT CAA AGT AGC AAT GTC TTC GCA TCC AAA CAG CTG GTC GCA AAC ATT Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln Leu Val Ala Asn Ile 1 5 10 15	48
TAT AAG CCC AAT CAG ATT CCA AGA GAA TTA ACT TCT CCT CAG GCG TTA Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr Ser Pro Gln Ala Leu 20 25 30	96
CCA TTA TCG CCC ATC ACC TCA CCA ATT CTC AAT TAC CAA CCA TTA TCA Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn Tyr Gln Pro Leu Ser 35 40 45	144
AAC TCC CCG CCT CCA GAT TTT GAT TTT GAT CTA GCT AAG CGC GGC GCA Asn Ser Pro Pro Pro Asp Phe Asp Phe Asp Leu Ala Lys Arg Gly Ala 50 55 60	192
GCC GAT TCT CAT GCT ATT CCT GTG GAT CCT CCA TCA TAT TTT GAT GTA Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro Ser Tyr Phe Asp Val 65 70 75 80	240
TTA AAG GCC GAT GGG ATT GAA TTG CCA TAC TAC GAT ACA AGT TCA TCT Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr Asp Thr Ser Ser Ser 85 90 95	288
AAA ATT CCT GAA CTA AAA CTA AAC AAA TCT AGA GAG ACA TTG GCC AGC Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg Glu Thr Leu Ala Ser 100 105 110	336
ATT GAG GAG GAC TCA TTC AAT GGT TGG TCT CAA ATT GAT GAC TTA TCC Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln Ile Asp Asp Leu Ser 115 120 125	384
GAC GAA GAT GAC AAT GAT GGC GAT ATA GCA TCT GGT TTC AAC TTC AAG Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser Gly Phe Asn Phe Lys 130 135 140	432
CTG TCA ACC AGT GCT CCG AGT GAG AAC GTT AAT TCA CAC ACT CCT ATT Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn Ser His Thr Pro Ile 145 150 155 160	480
TTG CAG TCT TTA AAC ATG AGT CTT GAT GGG AGA AAA AAA AAT CGT GCC Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg Lys Lys Asn Arg Ala 165 170 175	528
AGT CTA CAC GCA ACA TCA GTG TTA CCT AGT ACA ATA AGA CAG AAC AAT Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr Ile Arg Gln Asn Asn 180 185 190	576
CAG CAT TTC AAT GAC ATA AAC CAG ATG CTA GGC AGT AGT GAC GAA GAT Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly Ser Ser Asp Glu Asp 195 200 205	624
GCC TTT CCC AAA AGC CAA TCA TTA AAT TTC AAT AAG AAA CTA CCA ATA Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn Lys Lys Leu Pro Ile 210 215 220	672
CTT AAA ATT AAT GAT AAC GTC ATA CAA TCA AAC AGC AAT AGT AAT AAC Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn Ser Asn Ser Asn Asn 225 230 235 240	720
AGA GTT GAT AAT CCA GAA GAT ACA GTG GAT TCT TCA GTC GAT ATT ACA Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser Ser Val Asp Ile Thr 245 250 255	768

40

GCA TTT TAT GAT CCA AGA ATG TCA TCA GAT TCC AAA TTT GAT TGG GAG	816
Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser Lys Phe Asp Trp Glu	
260 265 270	
GTA AGC AAG AAC CAT GTT GAC CCA GCA GCC TAC TCG GTT AAC GTT GCT	864
Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr Ser Val Asn Val Ala	
275 280 285	
AGT GAA AAC CGT GTA CTG GAC GAC TTT AAG AAA GCA TTT CGC GAA AAG	912
Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys Ala Phe Arg Glu Lys	
290 295 300	
AGA AAA TAAGTACATT ATTTTCATTC TCCGACAGAA TTGCTACCAT TTTACTTTGT	968
Arg Lys	
305	
GTCCTGTGAT TCAATAGTGT ACAATATATT GGACATTTTA TAGTATACAA ATATACACCA	1028
TCAATCTATA CATCCATATC ACTTGTCGTA AAGATATCCC TTTTAATAG TACAGCGATT	1088
AAAAAATAA CATGATTAAC GTTCAGTTAC CAATGAGCTT ATTTATTAGG CTTGCTTTAG	1148
ATTTTCCAA GTCAATTTTT GTTTTTTCTA ACGCTTGCAA CCTCATCTCA ACCTTCTTCC	1208
TTTGCAAGCA GATC	1222

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln Leu Val Ala Asn Ile	
1 5 10 15	
Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr Ser Pro Gln Ala Leu	
20 25 30	
Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn Tyr Gln Pro Leu Ser	
35 40 45	
Asn Ser Pro Pro Pro Asp Phe Asp Phe Asp Leu Ala Lys Arg Gly Ala	
50 55 60	
Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro Ser Tyr Phe Asp Val	
65 70 75 80	
Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr Asp Thr Ser Ser Ser	
85 90 95	
Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg Glu Thr Leu Ala Ser	
100 105 110	
Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln Ile Asp Asp Leu Ser	
115 120 125	
Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser Gly Phe Asn Phe Lys	
130 135 140	
Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn Ser His Thr Pro Ile	
145 150 155 160	

41

Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg Lys Lys Asn Arg Ala  
                   165                  170                  175  
 Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr Il Arg Gln Asn Asn  
                   180                  185                  190  
 Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly Ser Ser Asp Glu Asp  
                   195                  200                  205  
 Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn Lys Lys Leu Pro Ile  
                   210                  215                  220  
 Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn Ser Asn Ser Asn Asn  
                   225                  230                  235                  240  
 Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser Ser Val Asp Ile Thr  
                   245                  250                  255  
 Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser Lys Phe Asp Trp Glu  
                   260                  265                  270  
 Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr Ser Val Asn Val Ala  
                   275                  280                  285  
 Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys Ala Phe Arg Glu Lys  
                   290                  295                  300  
 Arg Lys  
 305

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CINC coding sequence

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCAAAGTA GCAATGTCTT CGCATCCAAA CAGCTGGTCG CAAACATTTA TAAGCCCAAT	60
CA ATTCCAA GAGAATTAAC TTCTCCTCAG GCGTTACCAT TATCGCCCAT CACCTCACCA	120
ATTCTCAATT ACCAACCATT ATCAAACCTCC CCGCCTCCAG ATTTTGATTT TGATCTAGCT	180
AAGCGCGGCG CAGCCGATTC TCATGCTATT CCTGTGGATC CTCCATCATA TTTTGATGTA	240
TTAAAGGCCG ATGGGATTGA ATTGCCATAC TACGATACAA GTTCATCTAA AATTCCTGAA	300
CTAAACTAA ACAAATCTAG AGAGACATTG GCCAGCATTG AGGAGGACTC ATTCAATGGT	360
TGGTCTCAAA TTGATGACTT ATCCGACGAA GATGACAATG ATGGCGATAT AGCATCTGGT	420
TTCAACTTCA AGCTGTCAAC CAGTGCTCCG AGTGAGAACG TTAATTCACA CACTCCTATT	480
TTGCAGTCTT TAAACATGAG TCTTGATGGG AGAAAAAAA ATCGTGCCAG TCTACACGCA	540

42

```

ACATCAGTGT TACCTAGTAC AATAAGACAG AACAAATCAGC ATTTCAATGA CATAAACCAG      600
ATGCTAGGCA GTAGTGACGA AGATGCCTTT CCCAAAAGCC AATCATTAAA TTTCAATAAG      660
AAACTACCAA TACTTAAAAT TAATGATAAC GTCATACAAT CAAACAGCAA TAGTAATAAC      720
AGAGTTGATA ATCCAGAAGA TACAGTGGAT TCTTCAGTCG ATATTACAGC ATTTTATGAT      780
CCAAGAATGT CATCAGATTC CAAATTTGAT TGGGAGGTAA GCAAGAACCA TGTTGACCCA      840
GCAGCCTACT CGGTTAACGT TGCTAGTGAA AACCGTGTAC TGGACGACTT TAAGAAAGCA      900
TTTCGCGAAA AGAGAAAA                      918

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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: genomic DNA fragment containing full CNI coding sequence

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 376..3120

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CCGAACACTT CCTTCGAGAG AGTGCATTTT ACTATGTGAA CCAATTTTTC CTCTTTTTCG      60
GTTTGCAAGT TCACCTGAAA AACTGCTTAA CACTACTAGC AATTGCCCTA TTGTCGTACG      120
AGGACTTTGC CAAATGTATT CCCGGCTGTT TGTAGTATAT ATACGCAGAT ATATAATAGC      180
GCCGTCTTTT TACCTCTTTG AGCGAATTGC CAAATATTGA CTCTTTTGTC TTATTTGCT      240
ATCCCCATCT TATCAAAAAT GGGAACAACCT CGTTGAAATA AGAGACAAGC AACAAGAAAG      300
ACAACCAACA GAAAGTTCCA TTCCGCACAA ATACGCTGGA ATCCCATAGA ATATTGCTTG      360
TTCCTCTATG ACTAC ATG CTC CAA TTC AAT ACA GAA AAT GAT ACT GTA GCT      411
          Met Leu Gln Phe Asn Thr Glu Asn Asp Thr Val Ala
            1             5             10

CCA GTG TTT CCC ATG GAG CAA GAT ATA AAT GCA GCA CCT GAT GCC GTC      459
Pro Val Phe Pro Met Glu Gln Asp Ile Asn Ala Ala Pro Asp Ala Val
          15             20             25

CCA CTG GTG CAG ACA ACA ACA CTA CAA GTC TTT GTA AAG CTT GCC GAA      507
Pro Leu Val Gln Thr Thr Thr Leu Gln Val Phe Val Lys Leu Ala Glu
          30             35             40

CCC ATA GTG TTT TTA AAA GGA TTT GAA ACT AAC GGA CTG TCT GAA ATA      555
Pro Il Val Phe Leu Lys Gly Phe Glu Thr Asn Gly Leu Ser Glu Ile
          45             50             55             60

```

43

GCC	CCC	AGT	ATC	TTA	CGA	GGA	TCT	CTT	ATC	GTC	AGG	GTG	TTG	AAA	CCG	603
Ala	Pro	Ser	Ile	Leu	Arg	Gly	Ser	Leu	Ile	Val	Arg	Val	Leu	Lys	Pro	
				65					70					75		
AAT	AAA	TTA	AAA	AGT	ATA	TCG	ATA	ACC	TTC	AAA	GGA	ATA	TCC	AGA	ACA	651
Asn	Lys	Leu	Lys	Ser	Ile	Ser	Ile	Thr	Phe	Lys	Gly	Ile	Ser	Arg	Thr	
			80					85					90			
GAG	TGG	CCG	GAA	GGT	ATA	CCA	CCG	AAG	AGA	GAA	GAA	TTT	TCA	GAT	GTT	699
Glu	Trp	Pro	Glu	Gly	Ile	Pro	Pro	Lys	Arg	Glu	Glu	Phe	Ser	Asp	Val	
		95					100					105				
GAA	ACT	GTT	GTC	AAT	CAC	ACA	TGG	CCA	TTT	TAT	CAG	GCG	GAT	GAC	GGC	747
Glu	Thr	Val	Val	Asn	His	Thr	Trp	Pro	Phe	Tyr	Gln	Ala	Asp	Asp	Gly	
	110					115					120					
ATG	AAT	TCT	TTC	ACC	TTA	GAA	CAT	CAC	AGC	TCA	AAT	AAT	TCG	TCC	AAT	795
Met	Asn	Ser	Phe	Thr	Leu	Glu	His	His	Ser	Ser	Asn	Asn	Ser	Ser	Asn	
	125				130					135					140	
CGC	CCA	TCT	ATG	AGC	GAT	GAA	GAT	TAT	CTA	CTT	GAA	AAA	AGC	GGT	GCT	843
Arg	Pro	Ser	Met	Ser	Asp	Glu	Asp	Tyr	Leu	Leu	Glu	Lys	Ser	Gly	Ala	
				145					150					155		
TCA	GTA	TAT	ATC	CCA	CCA	ACC	GCT	GAA	CCC	CCT	AAA	GAT	AAT	AGC	AAT	891
Ser	Val	Tyr	Ile	Pro	Pro	Thr	Ala	Glu	Pro	Pro	Lys	Asp	Asn	Ser	Asn	
			160					165					170			
CTA	AGT	CTG	GAT	GCC	TAT	GAG	CGC	AAC	TCA	TTG	TCA	TCC	GAT	AAT	TTG	939
Leu	Ser	Leu	Asp	Ala	Tyr	Glu	Arg	Asn	Ser	Leu	Ser	Ser	Asp	Asn	Leu	
		175					180					185				
AGT	AAC	AAG	CCA	GTA	TCA	AGT	GAT	GTT	TCC	CAT	GAC	GAC	AGT	AAA	CTG	987
Ser	Asn	Lys	Pro	Val	Ser	Ser	Asp	Val	Ser	His	Asp	Asp	Ser	Lys	Leu	
	190					195					200					
TTG	GCT	ATT	CAA	AAG	ACA	CCA	TTA	CCA	TCA	TCT	AGT	CGA	AGA	GGA	TCG	1035
Leu	Ala	Ile	Gln	Lys	Thr	Pro	Leu	Pro	Ser	Ser	Ser	Arg	Arg	Gly	Ser	
	205				210					215				220		
GTA	CCG	GCA	AAT	TTT	CAC	GGT	AAC	TCT	TTG	TCA	CCT	CAT	ACC	TTC	ATA	1083
Val	Pro	Ala	Asn	Phe	His	Gly	Asn	Ser	Leu	Ser	Pro	His	Thr	Phe	Ile	
				225					230					235		
TCT	GAT	TTG	TTC	ACA	AAA	ACA	TTC	AGT	AAT	AGT	GGC	GCT	ACT	CCA	AGT	1131
Ser	Asp	Leu	Phe	Thr	Lys	Thr	Phe	Ser	Asn	Ser	Gly	Ala	Thr	Pro	Ser	
			240				245						250			
CCT	GAG	CAA	GAG	GAT	AAC	TAT	CTT	ACA	CCA	TCC	AAA	GAT	TCT	AAA	GAA	1179
Pro	Glu	Gln	Glu	Asp	Asn	Tyr	Leu	Thr	Pro	Ser	Lys	Asp	Ser	Lys	Glu	
		255					260					265				
GTT	TTT	ATT	TTT	CGA	CCG	GGC	GAT	TAT	ATT	TAC	ACT	TTT	GAA	CAG	CCA	1227
Val	Phe	Ile	Phe	Arg	Pro	Gly	Asp	Tyr	Ile	Tyr	Thr	Phe	Glu	Gln	Pro	
	270					275					280					
ATA	TCG	CAA	TCT	TAT	CCA	GAA	AGT	ATA	AAA	GCC	AAT	TTT	GGT	TCC	GTG	1275
Ile	Ser	Gln	Ser	Tyr	Pro	Glu	Ser	Ile	Lys	Ala	Asn	Phe	Gly	Ser	Val	
	285				290					295					300	
GAG	TAT	AAA	CTG	TCA	ATA	GAC	ATA	GAG	AGG	TTT	GGC	GCA	TTC	AAA	TCA	1323
Glu	Tyr	Lys	Leu	Ser	Ile	Asp	Ile	Glu	Arg	Phe	Gly	Ala	Phe	Lys	Ser	
				305					310					315		
ACT	ATA	CAT	ACT	CAA	TTA	CCC	ATC	AAA	GTC	GTA	AGG	CTT	CCT	TCT	GAT	1371
Thr	Ile	His	Thr	Gln	Leu	Pro	Ile	Lys	Val	Val	Arg	Leu	Pro	Ser	Asp	
			320					325					330			

GGA	TCC	GTA	GAA	GAG	ACT	GAA	GCT	ATT	GCA	ATT	TCC	AAG	GAC	TGG	AAA	1419
Gly	Ser	Val	Glu	Glu	Thr	Glu	Ala	Ile	Ala	Ile	Ser	Lys	Asp	Trp	Lys	
		335					340					345				
GAT	CTT	CTT	CAT	TAT	GAC	GTG	GTA	ATT	TTC	TCG	AAA	GAG	ATC	GTT	TTG	1467
Asp	Leu	Leu	His	Tyr	Asp	Val	Val	Ile	Phe	Ser	Lys	Glu	Ile	Val	Leu	
	350					355					360					
AAT	GCA	TTT	TTA	CCC	ATC	GAT	TTC	CAT	TTC	GCT	CCT	CTA	GAT	AAA	GTT	1515
Asn	Ala	Phe	Leu	Pro	Ile	Asp	Phe	His	Phe	Ala	Pro	Leu	Asp	Lys	Val	
	365				370					375					380	
ACT	CTG	CAT	CGT	ATT	AGA	ATT	TAT	CTA	ACA	GAG	TCT	ATG	GAA	TAC	ACT	1563
Thr	Leu	His	Arg	Ile	Arg	Ile	Tyr	Leu	Thr	Glu	Ser	Met	Glu	Tyr	Thr	
			385						390					395		
TGT	AAT	AGT	AAT	GGA	AAT	CAC	GAG	AAG	GCT	CGT	AGA	TTA	GAG	CCA	ACT	1611
Cys	Asn	Ser	Asn	Gly	Asn	His	Glu	Lys	Ala	Arg	Arg	Leu	Glu	Pro	Thr	
			400					405					410			
AAA	AAG	TTT	CTG	TTG	GCT	GAA	CAT	AAC	GGT	CCT	AAA	CTG	CCT	CAT	ATA	1659
Lys	Lys	Phe	Leu	Leu	Ala	Glu	His	Asn	Gly	Pro	Lys	Leu	Pro	His	Ile	
		415					420					425				
CCA	GCT	GGT	TCG	AAT	CCT	TTG	AAG	GCT	AAA	AAT	AGA	GGG	AAC	ATC	CTC	1707
Pro	Ala	Gly	Ser	Asn	Pro	Leu	Lys	Ala	Lys	Asn	Arg	Gly	Asn	Ile	Leu	
	430					435					440					
TTG	GAT	GAA	AAA	TCC	GGC	GAT	CTA	GTT	AAC	AAA	GAT	TTT	CAG	TTC	GAG	1755
Leu	Asp	Glu	Lys	Ser	Gly	Asp	Leu	Val	Asn	Lys	Asp	Phe	Gln	Phe	Glu	
	445				450					455					460	
GTG	TTT	GTC	CCA	AGC	AAG	TTT	ACA	AAC	AGT	ATA	CGG	TTA	CAC	CCT	GAT	1803
Val	Phe	Val	Pro	Ser	Lys	Phe	Thr	Asn	Ser	Ile	Arg	Leu	His	Pro	Asp	
				465					470					475		
ACA	AAT	TAT	GAT	AAA	ATC	AAA	GCC	CAC	CAT	TGG	ATA	AAA	ATT	TGC	CTT	1851
Thr	Asn	Tyr	Asp	Lys	Ile	Lys	Ala	His	His	Trp	Ile	Lys	Ile	Cys	Leu	
			480				485						490			
CGT	CTT	TCC	AAG	AAG	TAC	GGG	GAC	AAT	AGA	AAA	CAT	TTC	GAA	ATA	AGT	1899
Arg	Leu	Ser	Lys	Lys	Tyr	Gly	Asp	Asn	Arg	Lys	His	Phe	Glu	Ile	Ser	
		495				500						505				
ATT	GAT	TCT	CCA	ATC	CAT	ATT	TTA	AAT	CAA	CTA	TGC	TCA	CAC	GCG	AAT	1947
Ile	Asp	Ser	Pro	Ile	His	Ile	Leu	Asn	Gln	Leu	Cys	Ser	His	Ala	Asn	
	510					515					520					
ACT	TTG	CTA	CCG	AGC	TAC	GAG	AGT	CAT	TTC	CAG	TAT	TGT	GAT	GAA	GAT	1995
Thr	Leu	Leu	Pro	Ser	Tyr	Glu	Ser	His	Phe	Gln	Tyr	Cys	Asp	Glu	Asp	
	525				530					535					540	
GGT	AAT	TTC	GCA	CCA	GCA	GCA	GAT	CAA	CAA	AAT	TAC	GCA	AGT	CAT	CAT	2043
Gly	Asn	Phe	Ala	Pro	Ala	Ala	Asp	Gln	Gln	Asn	Tyr	Ala	Ser	His	His	
				545					550					555		
GAT	TCC	AAT	ATT	TTC	TTC	CCA	AAA	GAA	GTT	CTT	TCG	TCT	CCC	GTT	CTT	2091
Asp	Ser	Asn	Ile	Phe	Phe	Pro	Lys	Glu	Val	Leu	Ser	Ser	Pro	Val	Leu	
			560					565					570			
TCA	CCT	AAC	GTG	CAG	AAG	ATG	AAC	ATT	AGA	ATA	CCG	TCT	GAT	CTT	CCA	2139
Ser	Pr	Asn	Val	Gln	Lys	Met	Asn	Ile	Arg	Ile	Pro	Ser	Asp	Leu	Pro	
		575					580					585				
GTA	GTG	CGT	AAT	AGA	GCT	GAA	AGC	GTA	AAG	AAA	AGC	AAG	TCA	GAT	AAT	2187
Val	Val	Arg	Asn	Arg	Ala	Glu	Ser	Val	Lys	Lys	Ser	Lys	Ser	Asp	Asn	
		590				595					600					

45

ACC TCC AAG AAG AAT GAT CAA AGT AGC AAT GTC TTC GCA TCC AAA CAG Thr Ser Lys Lys Asn Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln 605 610 615 620	2235
CTG GTC GCA AAC ATT TAT AAG CCC AAT CAG ATT CCA AGA GAA TTA ACT Leu Val Ala Asn Ile Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr 625 630 635	2283
TCT CCT CAG GCG TTA CCA TTA TCG CCC ATC ACC TCA CCA ATT CTC AAT Ser Pro Gln Ala Leu Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn 640 645 650	2331
TAC CAA CCA TTA TCA AAC TCC CCG CCT CCA GAT TTT GAT TTT GAT CTA Tyr Gln Pro Leu Ser Asn Ser Pro Pro Asp Phe Asp Phe Asp Leu 655 660 665	2379
GCT AAG CGC GGC GCA GCC GAT TCT CAT GCT ATT CCT GTG GAT CCT CCA Ala Lys Arg Gly Ala Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro 670 675 680	2427
TCA TAT TTT GAT GTA TTA AAG GCC GAT GGG ATT GAA TTG CCA TAC TAC Ser Tyr Phe Asp Val Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr 685 690 695 700	2475
GAT ACA AGT TCA TCT AAA ATT CCT GAA CTA AAA CTA AAC AAA TCT AGA Asp Thr Ser Ser Ser Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg 705 710 715	2523
GAG ACA TTG GCC AGC ATT GAG GAG GAC TCA TTC AAT GGT TGG TCT CAA Glu Thr Leu Ala Ser Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln 720 725 730	2571
ATT GAT GAC TTA TCC GAC GAA GAT GAC AAT GAT GGC GAT ATA GCA TCT Ile Asp Asp Leu Ser Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser 735 740 745	2619
GGT TTC AAC TTC AAG CTG TCA ACC AGT GCT CCG AGT GAG AAC GTT AAT Gly Phe Asn Phe Lys Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn 750 755 760	2667
TCA CAC ACT CCT ATT TTG CAG TCT TTA AAC ATG AGT CTT GAT GGG AGA Ser His Thr Pro Ile Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg 765 770 775 780	2715
AAA AAA AAT CGT GCC AGT CTA CAC GCA ACA TCA GTG TTA CCT AGT ACA Lys Lys Asn Arg Ala Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr 785 790 795	2763
ATA AGA CAG AAC AAT CAG CAT TTC AAT GAC ATA AAC CAG ATG CTA GGC Ile Arg Gln Asn Asn Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly 800 805 810	2811
AGT AGT GAC GAA GAT GCC TTT CCC AAA AGC CAA TCA TTA AAT TTC AAT S r Ser Asp Glu Asp Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn 815 820 825	2859
AAG AAA CTA CCA ATA CTT AAA ATT AAT GAT AAC GTC ATA CAA TCA AAC Lys Lys Leu Pro Ile Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn 830 835 840	2907
AGC AAT AGT AAT AAC AGA GTT GAT AAT CCA GAA GAT ACA GTG GAT TCT Ser Asn Ser Asn Asn Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser 845 850 855 860	2955

46

TCA GTC GAT ATT ACA GCA TTT TAT GAT CCA AGA ATG TCA TCA GAT TCC	3003
Ser Val Asp Ile Thr Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser	
865 870 875	
AAA TTT GAT TGG GAG GTA AGC AAG AAC CAT GTT GAC CCA GCA GCC TAC	3051
Lys Phe Asp Trp Glu Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr	
880 885 890	
TCG GTT AAC GTT GCT AGT GAA AAC CGT GTA CTG GAC GAC TTT AAG AAA	3099
Ser Val Asn Val Ala Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys	
895 900 905	
GCA TTT CGC GAA AAG AGA AAA TAAGTACATT ATTTTCATTC TCCGACAGAA	3150
Ala Phe Arg Glu Lys Arg Lys	
910 915	
TTGCTACCAT TTTACTTTGT GTCCTGTGAT TCAATAGTGT ACAATATATT GGACATTTTA	3210
TAGTATACAA ATATACACCA TCAATCTATA CATCCATATC ACTTGTCGTA AAGATATCCC	3270
TTTTTAATAG TACAGCGATT AAAAAATAA CATGATTAAC GTTCAGTTAC CAATGAGCTT	3330
ATTTATTAGG CTTGCTTTAG ATTTTCCAA GTCAATTTTT GTTTTTTCTA ACGCTTGCAA	3390
CCTCATCTCA ACCTTCTTCC TTGCAAGCA GATCTTCGAA ACCATCTCGT TTATTCTCTC	3450
AATGCTGTTT CCACCTTCAT CATCGTCTGG GAAAAGTACC GGTAAGGGCG	3500

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Gln	Phe	Asn	Thr	Glu	Asn	Asp	Thr	Val	Ala	Pro	Val	Phe	Pro
1				5					10					15	
Met	Glu	Gln	Asp	Ile	Asn	Ala	Ala	Pro	Asp	Ala	Val	Pro	Leu	Val	Gln
			20					25					30		
Thr	Thr	Thr	Leu	Gln	Val	Phe	Val	Lys	Leu	Ala	Glu	Pro	Ile	Val	Phe
		35					40					45			
Leu	Lys	Gly	Phe	Glu	Thr	Asn	Gly	Leu	Ser	Glu	Ile	Ala	Pro	Ser	Ile
	50					55					60				
Leu	Arg	Gly	Ser	Leu	Ile	Val	Arg	Val	Leu	Lys	Pro	Asn	Lys	Leu	Lys
65					70					75					80
Ser	Ile	Ser	Ile	Thr	Phe	Lys	Gly	Ile	Ser	Arg	Thr	Glu	Trp	Pro	Glu
				85					90					95	
Gly	Ile	Pro	Pro	Lys	Arg	Glu	Glu	Phe	Ser	Asp	Val	Glu	Thr	Val	Val
			100					105					110		
Asn	His	Thr	Trp	Pro	Phe	Tyr	Gln	Ala	Asp	Asp	Gly	Met	Asn	Ser	Phe
		115					120					125			
Thr	Leu	Glu	His	His	Ser	Ser	Asn	Asn	Ser	Ser	Asn	Arg	Pr	Ser	Met
	130					135					140				



47

Ser Asp Glu Asp Tyr Leu Leu Glu Lys Ser Gly Ala Ser Val Tyr Ile  
 145 150 155 160  
 Pro Pro Thr Ala Glu Pro Pro Lys Asp Asn Ser Asn Leu Ser Leu Asp  
 165 170 175  
 Ala Tyr Glu Arg Asn Ser Leu Ser Ser Asp Asn Leu Ser Asn Lys Pro  
 180 185 190  
 Val Ser Ser Asp Val Ser His Asp Asp Ser Lys Leu Leu Ala Ile Gln  
 195 200 205  
 Lys Thr Pro Leu Pro Ser Ser Ser Arg Arg Gly Ser Val Pro Ala Asn  
 210 215 220  
 Phe His Gly Asn Ser Leu Ser Pro His Thr Phe Ile Ser Asp Leu Phe  
 225 230 235 240  
 Thr Lys Thr Phe Ser Asn Ser Gly Ala Thr Pro Ser Pro Glu Gln Glu  
 245 250 255  
 Asp Asn Tyr Leu Thr Pro Ser Lys Asp Ser Lys Glu Val Phe Ile Phe  
 260 265 270  
 Arg Pro Gly Asp Tyr Ile Tyr Thr Phe Glu Gln Pro Ile Ser Gln Ser  
 275 280 285  
 Tyr Pro Glu Ser Ile Lys Ala Asn Phe Gly Ser Val Glu Tyr Lys Leu  
 290 295 300  
 Ser Ile Asp Ile Glu Arg Phe Gly Ala Phe Lys Ser Thr Ile His Thr  
 305 310 315 320  
 Gln Leu Pro Ile Lys Val Val Arg Leu Pro Ser Asp Gly Ser Val Glu  
 325 330 335  
 Glu Thr Glu Ala Ile Ala Ile Ser Lys Asp Trp Lys Asp Leu Leu His  
 340 345 350  
 Tyr Asp Val Val Ile Phe Ser Lys Glu Ile Val Leu Asn Ala Phe Leu  
 355 360 365  
 Pro Ile Asp Phe His Phe Ala Pro Leu Asp Lys Val Thr Leu His Arg  
 370 375 380  
 Ile Arg Ile Tyr Leu Thr Glu Ser Met Glu Tyr Thr Cys Asn Ser Asn  
 385 390 395 400  
 Gly Asn His Glu Lys Ala Arg Arg Leu Glu Pro Thr Lys Lys Phe Leu  
 405 410 415  
 Leu Ala Glu His Asn Gly Pro Lys Leu Pro His Ile Pro Ala Gly Ser  
 420 425 430  
 Asn Pro Leu Lys Ala Lys Asn Arg Gly Asn Ile Leu Leu Asp Glu Lys  
 435 440 445  
 Ser Gly Asp Leu Val Asn Lys Asp Phe Gln Phe Glu Val Phe Val Pro  
 450 455 460  
 Ser Lys Phe Thr Asn Ser Ile Arg Leu His Pro Asp Thr Asn Tyr Asp  
 465 470 475 480  
 Lys Ile Lys Ala His His Trp Ile Lys Ile Cys L u Arg Leu Ser Lys  
 485 490 495

48

Lys Tyr Gly Asp Asn Arg Lys His Phe Glu Ile Ser Ile Asp Ser Pro  
 500 505 510  
 Ile His Ile Leu Asn Gln Leu Cys Ser His Ala Asn Thr Leu Leu Pro  
 515 520 525  
 Ser Tyr Glu Ser His Phe Gln Tyr Cys Asp Glu Asp Gly Asn Phe Ala  
 530 535 540  
 Pro Ala Ala Asp Gln Gln Asn Tyr Ala Ser His His Asp Ser Asn Ile  
 545 550 555 560  
 Phe Phe Pro Lys Glu Val Leu Ser Ser Pro Val Leu Ser Pro Asn Val  
 565 570 575  
 Gln Lys Met Asn Ile Arg Ile Pro Ser Asp Leu Pro Val Val Arg Asn  
 580 585 590  
 Arg Ala Glu Ser Val Lys Lys Ser Lys Ser Asp Asn Thr Ser Lys Lys  
 595 600 605  
 Asn Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln Leu Val Ala Asn  
 610 615 620  
 Ile Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr Ser Pro Gln Ala  
 625 630 635 640  
 Leu Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn Tyr Gln Pro Leu  
 645 650 655  
 Ser Asn Ser Pro Pro Pro Asp Phe Asp Phe Asp Leu Ala Lys Arg Gly  
 660 665 670  
 Ala Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro Ser Tyr Phe Asp  
 675 680 685  
 Val Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr Asp Thr Ser Ser  
 690 695 700  
 Ser Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg Glu Thr Leu Ala  
 705 710 715 720  
 Ser Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln Ile Asp Asp Leu  
 725 730 735  
 Ser Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser Gly Phe Asn Phe  
 740 745 750  
 Lys Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn Ser His Thr Pro  
 755 760 765  
 Ile Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg Lys Lys Asn Arg  
 770 775 780  
 Ala Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr Ile Arg Gln Asn  
 785 790 795 800  
 Asn Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly Ser Ser Asp Glu  
 805 810 815  
 Asp Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn Lys Lys Leu Pro  
 820 825 830  
 Ile Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn Ser Asn Ser Asn  
 835 840 845

49

Asn Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser Ser Val Asp Ile  
 850 855 860  
 Thr Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser Lys Phe Asp Trp  
 865 870 875 880  
 Glu Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr Ser Val Asn Val  
 885 890 895  
 Ala Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys Ala Phe Arg Glu  
 900 905 910  
 Lys Arg Lys  
 915

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: coding sequence of CNI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCTCCAAT TCAATACAGA AAATGATACT GTAGCTCCAG TGTTCCTCCAT GGAGCAAGAT	60
ATAAATGCAG CACCTGATGC CGTCCCCTG GTGCAGACAA CAACACTACA AGTCTTTGTA	120
AAGCTTGCCG AACCCATAGT GTTTTTAAAA GGATTTGAAA CTAACGGACT GTCTGAAATA	180
GCCCCAGTA TCTTACGAGG ATCTCTTATC GTCAGGGTGT TGAAACCGAA TAAATTAATA	240
AGTATATCGA TAACCTTCAA AGGAATATCC AGAACAGAGT GGCCGGAAGG TATACCACCG	300
AAGAGAGAAG AATTTTCAGA TGTGAAACT GTTGTCATC ACACATGGCC ATTTTATCAG	360
GCGGATGACG GCATGAATTC TTTCACCTTA GAACATCACA GCTCAAATAA TTCGTCCAAT	420
CGCCCATCTA TGAGCGATGA AGATTATCTA CTTGAAAAAA GCGGTGCTTC AGTATATATC	480
CCACCAACCG CTGAACCCCC TAAAGATAAT AGCAATCTAA GTCTGGATGC CTATGAGCGC	540
AACTCATTGT CATCCGATAA TTTGAGTAAC AAGCCAGTAT CAAGTGATGT TTCCCATGAC	600
GACAGTAAAC TGTTGGCTAT TCAAAAGACA CCATTACCAT CATCTAGTCG AAGAGGATCG	660
GTACGGGCAA ATTTTCACGG TAACTCTTTG TCACCTCATA CCTTCATATC TGATTTGTTC	720
ACAAAAACAT TCAGTAATAG TGGCGCTACT CCAAGTCCTG AGCAAGAGGA TAACTATCTT	780
ACACCATCCA AAGATTCTAA AGAAGTTTTT ATTTTTCGAC CGGGCGATTA TATTTACACT	840
TTTGAACAGC CAATATCGCA ATCTTATCCA GAAAGTATAA AAGCCAATTT TGGTTCCGTG	900
GAGTATAAAC TGTCAATAGA CATAGAGAGG TTTGGCGCAT TCAAATCAAC TATACATACT	960

CAATTACCCA	TCAAAGTCGT	AAGGCTTCCT	TCTGATGGAT	CCGTAGAAGA	GA CTGAAGCT	1020
ATTGCAATTT	CCAAGGACTG	GAAAGATCTT	CTTCATTATG	ACGTGGTAAT	TTTCTCGAAA	1080
GAGATCGTTT	TGAATGCATT	TTTACCCATC	GATTTCCTATT	TCGCTCCTCT	AGATAAAGTT	1140
ACTCTGCATC	GTATTAGAAT	TTATCTAACA	GAGTCTATGG	AATACACTTG	TAATAGTAAT	1200
GGAAATCACG	AGAAGGCTCG	TAGATTAGAG	CCAAC TAAAA	AGTTTCTGTT	GGCTGAACAT	1260
AACGGTCCTA	AACTGCCTCA	TATACCAGCT	GGTTCGAATC	CTTGAAGGC	TAAAAATAGA	1320
GGGAACATCC	TCTTGGATGA	AAAATCCGGC	GATCTAGTTA	ACAAAGATTT	TCAGTTCGAG	1380
GTGTTTGTCC	CAAGCAAGTT	TACAAACAGT	ATACGGTTAC	ACCCTGATAC	AAATTATGAT	1440
AAAATCAAAG	CCCACCATTG	GATAAAAATT	TGCCTTCGTC	TTCCAAGAA	GTACGGGGAC	1500
AATAGAAAAC	ATTTCGAAAT	AAGTATTGAT	TCTCCAATCC	ATATTTTAAA	TCAACTATGC	1560
TCACACGCGA	ATACTTTGCT	ACCGAGCTAC	GAGAGTCATT	TCCAGTATTG	TGATGAAGAT	1620
GGTAATTTTCG	CACCAGCAGC	AGATCAACAA	AATTACGCAA	GTCATCATGA	TTCCAATATT	1680
TTCTTCCCAA	AAGAAGTTCT	TTCGTCTCCC	GTTCTTTCAC	CTAACGTGCA	GAAGATGAAC	1740
ATTAGAATAC	CGTCTGATCT	TCCAGTAGTG	CGTAATAGAG	CTGAAAGCGT	AAAGAAAAGC	1800
AAGTCAGATA	ATACCTCCAA	GAAGAATGAT	CAAAGTAGCA	ATGTCTTCGC	ATCCAAACAG	1860
CTGGTCGCAA	ACATTTATAA	GCCCAATCAG	ATTCCAAGAG	AATTAAC TTC	TCCTCAGGCG	1920
TTACCATTAT	CGCCCATCAC	CTCACCAATT	CTCAATTACC	AACCATTATC	AAACTCCCCG	1980
CCTCCAGATT	TTGATTTTGA	TCTAGCTAAG	CGCGGCGCAG	CCGATTCTCA	TGCTATTCTT	2040
GTGGATCCTC	CATCATATTT	TGATGTATTA	AAGGCCGATG	GGATTGAATT	GCCATACTAC	2100
GATACAAGTT	CATCTAAAT	TCCTGAACTA	AACTAAACA	AATCTAGAGA	GACATTGGCC	2160
AGCATTGAGG	AGGACTCATT	CAATGGTTGG	TCTCAAATTG	ATGACTTATC	CGACGAAGAT	2220
GACAATGATG	GCGATATAGC	ATCTGGTTTC	AACTTCAAGC	TGTC AACCAG	TGCTCCGAGT	2280
GAGAACGTTA	ATTCACACAC	TCCTATTTTG	CAGTCTTTAA	ACATGAGTCT	TGATGGGAGA	2340
AAAAAAAATC	GTGCCAGTCT	ACACGCAACA	TCAGTGTTAC	CTAGTACAAT	AAGACAGAAC	2400
AATCAGCATT	TCAATGACAT	AAACCAGATG	CTAGGCAGTA	GTGACGAAGA	TGCCTTTCCC	2460
AAAAGCCAAT	CATTAAATTT	CAATAAGAAA	CTACCAATAC	TTAAAATTAA	TGATAACGTC	2520
ATACAATCAA	ACAGCAATAG	TAATAACAGA	GTTGATAATC	CAGAAGATAC	AGTGGATTCT	2580
TCAGTCGATA	TTACAGCATT	TTATGATCCA	AGAATGTCAT	CAGATTCCAA	ATTTGATTGG	2640
GAGGTAAGCA	AGAACCATGT	TGACCCAGCA	GCCTACTCGG	TTAACGTTGC	TAGTGAAAAC	2700
CGTG TACTGG	ACGACTTTAA	GAAAGCATT	CGCGAAAAGA	GAAAA		2745

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

51

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CNI-PRC-A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCAAAAAAG AGATCTCGGA TCAAAGTAGC

30

## (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CNI-PCR-B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGTTTTTCA GTGTCGACGA TTCATAGATC

30

## (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1964 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: genomic DNA fragment containing full  
CNA1 coding sequence

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 286..1944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTTGTGCA TTTTGATATT CATCTATATC TATTTCAAAA TTTTTCATGT CATCGCCTCT

60

52

TGAAACATGA ATTTTCCAAT TCTGAAAAAG AACGTACTAC TGGGAAACAA AAGGGAAAAA	120
TGTATAAATC CTTTAATGTT TTTGAATCAA GAGGCATTAT TATAAAAGAA CGAAGCAAAG	180
CCTTTAATAT TTGCTTTATT AAAGGTATTA TTCAAAGAAA AGTTTTTTTTA GATTCTTTTT	240
TTTTTGACGT ATTAGCTCAG CTGCCATAAA ACACTCTCAA CGCCA ATG TCG AAA	294
Met Ser Lys 1	
GAC TTG AAT TCT TCA CGC ATC AAA ATC ATT AAA CCT AAT GAC TCT TAC	342
Asp Leu Asn Ser Ser Arg Ile Lys Ile Ile Lys Pro Asn Asp Ser Tyr 5 10 15	
ATA AAG GTT GAC CGG AAA AAA GAT TTA ACA AAA TAC GAA TTA GAA AAC	390
Ile Lys Val Asp Arg Lys Lys Asp Leu Thr Lys Tyr Glu Leu Glu Asn 20 25 30 35	
GGT AAA GTA ATT TCT ACT AAG GAC CGA TCC TAC GCT TCT GTA CCT GCC	438
Gly Lys Val Ile Ser Thr Lys Asp Arg Ser Tyr Ala Ser Val Pro Ala 40 45 50	
ATA ACA GGA AAG ATA CCA AGT GAT GAG GAA GTA TTC GAC TCC AAG ACG	486
Ile Thr Gly Lys Ile Pro Ser Asp Glu Glu Val Phe Asp Ser Lys Thr 55 60 65	
GGA TTA CCT AAT CAT TCC TTT TTA AGA GAG CAT TTC TTT CAT GAG GGT	534
Gly Leu Pro Asn His Ser Phe Leu Arg Glu His Phe Phe His Glu Gly 70 75 80	
CGA CTT TCT AAG GAA CAG GCC ATA AAA ATC TTA AAT ATG TCA ACT GTA	582
Arg Leu Ser Lys Glu Gln Ala Ile Lys Ile Leu Asn Met Ser Thr Val 85 90 95	
GCA TTG AGT AAA GAA CCC AAT CTA CTA AAA CTC AAA GCG CCA ATT ACT	630
Ala Leu Ser Lys Glu Pro Asn Leu Leu Lys Leu Lys Ala Pro Ile Thr 100 105 110 115	
ATA TGT GGT GAT ATT CAC GGG CAG TAT TAT GAT TTA TTG AAA CTG TTT	678
Ile Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu Lys Leu Phe 120 125 130	
GAA GTT GGC GGT GAC CCC GCC GAA ATC GAC TAT TTA TTC TTG GGG GAT	726
Glu Val Gly Gly Asp Pro Ala Glu Ile Asp Tyr Leu Phe Leu Gly Asp 135 140 145	
TAT GTT GAT AGA GGT GCA TTC TCT TTT GAG TGT CTG ATT TAT TTG TAC	774
Tyr Val Asp Arg Gly Ala Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr 150 155 160	
TCC TTG AAG TTG AAT AAT TTA GGG AGA TTT TGG ATG CTA AGA GGT AAC	822
Ser Leu Lys Leu Asn Asn Leu Gly Arg Phe Trp Met Leu Arg Gly Asn 165 170 175	
CAT GAG TGT AAG CAC TTG ACC TCT TAT TTT ACT TTT AAG AAT GAG ATG	870
His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met 180 185 190 195	
TTG CAC AAA TAC GAT ATG GAA GTT TAC GAT GCT TGC TGC AGA TCA TTC	918
Leu His Lys Tyr Asp Met Glu Val Tyr Asp Ala Cys Cys Arg Ser Phe 200 205 210	
AAT GTC TTA CCA TTA GCA GCT TTA ATG AAC GGA CAA TAT TTT TGT GTG	966
Asn Val Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr Phe Cys Val 215 220 225	

## 53

CAT GGT GGT ATC TCT CCA GAG TTA AAA TCA GTA GAG GAT GTT AAT AAA His Gly Gly Ile Ser Pro Glu Leu Lys Ser Val Glu Asp Val Asn Lys 230 235 240	1014
ATT AAT AGA TTT CGA GAA ATC CCA TCT CGT GGT CTC ATG TGT GAC CTA Ile Asn Arg Phe Arg Glu Ile Pro Ser Arg Gly Leu Met Cys Asp Leu 245 250 255	1062
CTA TGG GCC GAT CCT GTC GAA AAT TAT GAT GAT GCA AGA GAT GGT AGC Leu Trp Ala Asp Pro Val Glu Asn Tyr Asp Asp Ala Arg Asp Gly Ser 260 265 270 275	1110
GAA TTT GAT CAG AGC GAG GAT GAA TTC GTA CCT AAC AGT TTG AGG GGT Glu Phe Asp Gln Ser Glu Asp Glu Phe Val Pro Asn Ser Leu Arg Gly 280 285 290	1158
TGC TCT TTC GCC TTC ACT TTT AAA GCA TCA TGC AAG TTT TTG AAG GCA Cys Ser Phe Ala Phe Thr Phe Lys Ala Ser Cys Lys Phe Leu Lys Ala 295 300 305	1206
AAT GGT TTG TTA TCT ATT ATT AGA GCA CAC GAA GCA CAG GAT GCT GGG Asn Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly 310 315 320	1254
TAC AGA ATG TAT AAA AAC AAT AAA GTA ACA GGC TTC CCG AGC TTA ATA Tyr Arg Met Tyr Lys Asn Asn Lys Val Thr Gly Phe Pro Ser Leu Ile 325 330 335	1302
ACC ATG TTC AGT GCG CCA AAC TAC CTG GAC ACA TAT CAT AAT AAA GCT Thr Met Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr His Asn Lys Ala 340 345 350 355	1350
GCT GTG TTA AAA TAT GAA GAA AAC GTC ATG AAC ATC AGG CAG TTT CAC Ala Val Leu Lys Tyr Glu Glu Asn Val Met Asn Ile Arg Gln Phe His 360 365 370	1398
ATG TCT CCG CAC CCT TAC TGG TTG CCT GAT TTT ATG GAT GTT TTC ACC Met Ser Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp Val Phe Thr 375 380 385	1446
TGG TCA CTA CCT TTT GTT GGC GAA AAA GTT ACT AGC ATG TTA GTG TCT Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Ser Met Leu Val Ser 390 395 400	1494
ATA TTA AAC ATA TGT AGT GAG CAG GAA CTT GAC CCA GAA TCG GAA CCC Ile Leu Asn Ile Cys Ser Glu Gln Glu Leu Asp Pro Glu Ser Glu Pro 405 410 415	1542
AAA GCT GCG GAG GAG ACT GTA AAG GCA AGA GCA AAC GCA ACT AAG GAG Lys Ala Ala Glu Glu Thr Val Lys Ala Arg Ala Asn Ala Thr Lys Glu 420 425 430 435	1590
ACC GGC ACC CCA TCT GAT GAA AAG GCG TCA TCA GCG ATA TTA GAA GAT Thr Gly Thr Pro Ser Asp Glu Lys Ala Ser Ser Ala Ile Leu Glu Asp 440 445 450	1638
GAA ACC CGA AGA AAG GCT TTG AGA AAT AAG ATA TTA GCT ATT GCT AAA Glu Thr Arg Arg Lys Ala Leu Arg Asn Lys Ile Leu Ala Ile Ala Lys 455 460 465	1686
GTT TCA AGA ATG TTT TCG GTG CTA AGA GAA GAG AGC GAA AAA GTG GAA Val Ser Arg Met Phe Ser Val Leu Arg Glu Glu Ser Glu Lys Val Glu 470 475 480	1734
TAT TTG AAA ACT ATG AAT GCC GGT GTC TTA CCT CGT GGT GCT CTA GCT Tyr Leu Lys Thr Met Asn Ala Gly Val Leu Pro Arg Gly Ala Leu Ala 485 490 495	1782

54

CGT GGG ACT GAA GGT TTG AAT GAA ACG CTA AGC ACT TTT GAA AAG GCT	1830
Arg Gly Thr Glu Gly Leu Asn Glu Thr Leu Ser Thr Phe Glu Lys Ala	
500 505 510 515	
AGA AAG GAA GAC CTT ATT AAT GAA AAA TTA CCA CCA TCT TTA TCG GAG	1878
Arg Lys Glu Asp Leu Ile Asn Glu Lys Leu Pro Pro Ser Leu Ser Glu	
520 525 530	
GTT GAA CAA GAG AAG ATT AAA TAC TAC GAA AAA ATA TTA AAG GGA GCG	1926
Val Glu Gln Glu Lys Ile Lys Tyr Tyr Glu Lys Ile Leu Lys Gly Ala	
535 540 545	
GAG AAA AAG CCA CAA CTG TGATAAATCT TCATTTTATT	1964
Glu Lys Lys Pro Gln Leu	
550	

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 553 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ser	Lys	Asp	Leu	Asn	Ser	Ser	Arg	Ile	Lys	Ile	Ile	Lys	Pro	Asn
1				5					10					15	
Asp	Ser	Tyr	Ile	Lys	Val	Asp	Arg	Lys	Lys	Asp	Leu	Thr	Lys	Tyr	Glu
			20					25					30		
Leu	Glu	Asn	Gly	Lys	Val	Ile	Ser	Thr	Lys	Asp	Arg	Ser	Tyr	Ala	Ser
			35					40					45		
Val	Pro	Ala	Ile	Thr	Gly	Lys	Ile	Pro	Ser	Asp	Glu	Glu	Val	Phe	Asp
			50					55					60		
Ser	Lys	Thr	Gly	Leu	Pro	Asn	His	Ser	Phe	Leu	Arg	Glu	His	Phe	Phe
						70				75					80
His	Glu	Gly	Arg	Leu	Ser	Lys	Glu	Gln	Ala	Ile	Lys	Ile	Leu	Asn	Met
				85					90					95	
Ser	Thr	Val	Ala	Leu	Ser	Lys	Glu	Pro	Asn	Leu	Leu	Lys	Leu	Lys	Ala
				100					105				110		
Pro	Ile	Thr	Ile	Cys	Gly	Asp	Ile	His	Gly	Gln	Tyr	Tyr	Asp	Leu	Leu
				115				120					125		
Lys	Leu	Phe	Glu	Val	Gly	Gly	Asp	Pro	Ala	Glu	Ile	Asp	Tyr	Leu	Phe
				130			135				140				
Leu	Gly	Asp	Tyr	Val	Asp	Arg	Gly	Ala	Phe	Ser	Phe	Glu	Cys	Leu	Ile
					150					155				160	
Tyr	Leu	Tyr	Ser	Leu	Lys	Leu	Asn	Asn	Leu	Gly	Arg	Phe	Trp	Met	Leu
				165					170					175	
Arg	Gly	Asn	His	Glu	Cys	Lys	His	Leu	Thr	Ser	Tyr	Phe	Thr	Phe	Lys
				180				185					190		
Asn	Glu	Met	Leu	His	Lys	Tyr	Asp	Met	Glu	Val	Tyr	Asp	Ala	Cys	Cys
		195					200					205			



55

Arg Ser Phe Asn Val Leu Pro Leu Ala Ala L u Met Asn Gly Gln Tyr  
 210 215 220  
 Phe Cys Val His Gly Gly Ile Ser Pro Glu Leu Lys Ser Val Glu Asp  
 225 230 235 240  
 Val Asn Lys Ile Asn Arg Phe Arg Glu Ile Pro Ser Arg Gly Leu Met  
 245 250 255  
 Cys Asp Leu Leu Trp Ala Asp Pro Val Glu Asn Tyr Asp Asp Ala Arg  
 260 265 270  
 Asp Gly Ser Glu Phe Asp Gln Ser Glu Asp Glu Phe Val Pro Asn Ser  
 275 280 285  
 Leu Arg Gly Cys Ser Phe Ala Phe Thr Phe Lys Ala Ser Cys Lys Phe  
 290 295 300  
 Leu Lys Ala Asn Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln  
 305 310 315 320  
 Asp Ala Gly Tyr Arg Met Tyr Lys Asn Asn Lys Val Thr Gly Phe Pro  
 325 330 335  
 Ser Leu Ile Thr Met Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr His  
 340 345 350  
 Asn Lys Ala Ala Val Leu Lys Tyr Glu Glu Asn Val Met Asn Ile Arg  
 355 360 365  
 Gln Phe His Met Ser Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp  
 370 375 380  
 Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Ser Met  
 385 390 395 400  
 Leu Val Ser Ile Leu Asn Ile Cys Ser Glu Gln Glu Leu Asp Pro Glu  
 405 410 415  
 Ser Glu Pro Lys Ala Ala Glu Glu Thr Val Lys Ala Arg Ala Asn Ala  
 420 425 430  
 Thr Lys Glu Thr Gly Thr Pro Ser Asp Glu Lys Ala Ser Ser Ala Ile  
 435 440 445  
 Leu Glu Asp Glu Thr Arg Arg Lys Ala Leu Arg Asn Lys Ile Leu Ala  
 450 455 460  
 Ile Ala Lys Val Ser Arg Met Phe Ser Val Leu Arg Glu Glu Ser Glu  
 465 470 475 480  
 Lys Val Glu Tyr Leu Lys Thr Met Asn Ala Gly Val Leu Pro Arg Gly  
 485 490 495  
 Ala Leu Ala Arg Gly Thr Glu Gly Leu Asn Glu Thr Leu Ser Thr Phe  
 500 505 510  
 Glu Lys Ala Arg Lys Glu Asp Leu Ile Asn Glu Lys Leu Pro Pro Ser  
 515 520 525  
 Leu Ser Glu Val Glu Gln Glu Lys Ile Lys Tyr Tyr Glu Lys Ile Leu  
 530 535 540  
 Lys Gly Ala Glu Lys Lys Pro Gln Leu  
 545 550

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: genomic DNA fragment containing full CNA2 coding sequence

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..2073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAGTCTATA ATACGTTTGA TACAGCTAGA TATCGCTAGC GCCAACATTG TCCCCCTCTC	60
TTGATCAATG CTTTTTTTCG GCCCGAGACA AATGAGAAAA TGTCCTAAAA ATACCTTTCA	120
TCAAGACTCC TATTTTTCCT TAGAAAAAAC ATATATCCAA CTGGAACAGT ATTAAGCCAA	180
TTGCTACGAT ACAAACAAAA GGAGATATTC CTTCCCTCCC ATAGAGTCAC ACAGGAGCCA	240
GTACTTCTTC TTGAACCCGC A ATG TCT TCA GAC GCT ATA AGA AAT ACT GAG	291
Met Ser Ser Asp Ala Ile Arg Asn Thr Glu	10
1 5	
CAG ATA AAC GCC GCT ATT AAA ATT ATA GAA AAC AAA ACA GAG CGT CCG	339
Gln Ile Asn Ala Ala Ile Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro	25
15 20	
CAA TCG TCC ACA ACC CCT ATA GAT TCG AAG GCT AGT ACA GTT GCT GCT	387
Gln Ser Ser Thr Thr Pro Ile Asp Ser Lys Ala Ser Thr Val Ala Ala	40
30 35	
GCT AAT TCC ACG GCC ACA GAA ACT TCC AGA GAC CTT ACA CAA TAT ACC	435
Ala Asn Ser Thr Ala Thr Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr	55
45 50	
CTA GAT GAC GGA AGA GTC GTA TCG ACA AAC CGC AGA ATA ATG AAT AAA	483
Leu Asp Asp Gly Arg Val Val Ser Thr Asn Arg Arg Ile Met Asn Lys	70
60 65	
GTG CCC GCC ATC ACG TCA CAT GTT CCT ACA GAT GAA GAG CTG TTC CAG	531
Val Pro Ala Ile Thr Ser His Val Pro Thr Asp Glu Glu Leu Phe Gln	90
75 80	
CCC AAT GGG ATA CCT CGT CAC GAA TTC CTA AGA GAT CAT TTC AAG CGC	579
Pro Asn Gly Ile Pro Arg His Glu Phe Leu Arg Asp His Phe Lys Arg	105
95 100	
GAG GGC AAA TTG TCG GCT GCG CAG GCG GCC AGG ATC GTT ACA CTT GCA	627
Glu Gly Lys Leu Ser Ala Ala Gln Ala Ala Arg Ile Val Thr Leu Ala	120
110 115	
ACG GAA CTC TTC AGC AAA GAA CCC AAC CTT ATA TCT GTT CCC GCC CCA	675
Thr Glu Leu Phe Ser Lys Glu Pro Asn Leu Ile Ser Val Pro Ala Pro	135
125 130	

57

ATC Ile	ACA Thr	GTT Val	TGC Cys	GGT Gly	GAT Asp	ATC Ile	CAT His	GGC Gly	CAG Gln	TAC Tyr	TTT Phe	GAC Asp	CTT Leu	TTG Leu	AAG Lys	723
140						145					150					
CTA Leu	TTC Phe	GAA Glu	GTT Val	GGC Gly	GGA Gly	GAT Asp	CCG Pro	GCC Ala	ACT Thr	ACA Thr	TCG Ser	TAT Tyr	TTG Leu	TTC Phe	TTG Leu	771
155					160					165					170	
GGA Gly	GAC Asp	TAT Tyr	GTC Val	GAC Asp	AGA Arg	GGG Gly	TCC Ser	TTT Phe	TCG Ser	TTT Phe	GAG Glu	TGT Cys	CTT Leu	ATT Ile	TAT Tyr	819
				175					180					185		
TTA Leu	TAT Tyr	TCT Ser	TTG Leu	AAG Lys	CTG Leu	AAT Asn	TTT Phe	AAC Asn	GAC Asp	CAT His	TTC Phe	TGG Trp	CTA Leu	CTG Leu	AGG Arg	867
			190				195						200			
GGT Gly	AAC Asn	CAC His	GAA Glu	TGT Cys	AAG Lys	CAT His	CTA Leu	ACG Thr	TCA Ser	TAT Tyr	TTC Phe	ACT Thr	TTC Phe	AAA Lys	AAT Asn	915
		205					210					215				
GAA Glu	ATG Met	CTG Leu	CAC His	AAG Lys	TAC Tyr	AAT Asn	CTA Leu	GAT Asp	ATT Ile	TAC Tyr	GAG Glu	AAA Lys	TGC Cys	TGC Cys	GAA Glu	963
	220					225					230					
TCG Ser	TTT Phe	AAC Asn	AAC Asn	TTG Leu	CCC Pro	CTG Leu	GCT Ala	GCG Ala	TTA Leu	ATG Met	AAC Asn	GGA Gly	CAG Gln	TAT Tyr	CTT Leu	1011
235					240					245					250	
TGT Cys	GTT Val	CAT His	GGT Gly	GGT Gly	ATA Ile	TCT Ser	CCC Pro	GAG Glu	TTA Leu	AAC Asn	TCT Ser	TTA Leu	CAG Gln	GAC Asp	ATT Ile	1059
				255					260					265		
AAC Asn	AAC Asn	CTA Leu	AAT Asn	AGA Arg	TTC Phe	AGG Arg	GAG Glu	ATT Ile	CCC Pro	TCT Ser	CAT His	GGC Gly	CTG Leu	ATG Met	TGT Cys	1107
			270					275					280			
GAT Asp	CTG Leu	TTG Leu	TGG Trp	GCT Ala	GAC Asp	CCG Pro	ATT Ile	GAA Glu	GAG Glu	TAC Tyr	GAC Asp	GAA Glu	GTC Val	TTG Leu	GAT Asp	1155
			285				290					295				
AAA Lys	GAC Asp	TTG Leu	ACT Thr	GAG Glu	GAA Glu	GAC Asp	ATA Ile	GTG Val	AAC Asn	TCC Ser	AAA Lys	ACC Thr	ATG Met	GTT Val	CCT Pro	1203
	300					305					310					
CAT His	CAT His	GGC Gly	AAG Lys	ATG Met	GCA Ala	CCT Pro	TCA Ser	AGG Arg	GAT Asp	ATG Met	TTT Phe	GTC Val	CCA Pro	AAC Asn	TCA Ser	1251
	315				320					325					330	
GTA Val	AGG Arg	GGC Gly	TGT Cys	TCA Ser	TAT Tyr	GCC Ala	TTC Phe	ACG Thr	TAT Tyr	CGT Arg	GCT Ala	GCG Ala	TGC Cys	CAT His	TTT Phe	1299
				335					340					345		
CTG Leu	CAA Gln	GAG Glu	ACT Thr	GGC Gly	CTG Leu	TTG Leu	TCC Ser	ATC Ile	ATC Ile	AGG Arg	GCA Ala	CAC His	GAG Glu	GCT Ala	CAA Gln	1347
			350					355					360			
GAC Asp	GCT Ala	GGT Gly	TAT Tyr	AGA Arg	ATG Met	TAC Tyr	AAA Lys	AAT Asn	ACC Thr	AAG Lys	ACT Thr	TTG Leu	GGC Gly	TTT Phe	CCC Pro	1395
		365					370					375				
TCT Ser	CTT Leu	TTG Leu	ACC Thr	CTT Leu	TTC Phe	AGT Ser	GCG Ala	CCT Pro	AAC Asn	TAC Tyr	TTG Leu	GAC Asp	ACC Thr	TAC Tyr	AAT Asn	1443
	380					385					390					
AAT Asn	AAG Lys	GCT Ala	GCC Ala	ATA Ile	TTG Leu	AAA Lys	TAC Tyr	GAA Glu	AAT Asn	AAT Asn	GTT Val	ATG Met	AAT Asn	ATC Ile	AGA Arg	1491
	395				400					405					410	

58

CAA TTC AAC ATG ACT CCA CAC CCC TAT TGG TTA CCA GAT TTC ATG GAC	1539
Gln Phe Asn Met Thr Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp	
415 420 425	
GTT TTC ACG TGG TCC TTG CCA TTT GTT GGT GAA AAA GTT ACA GAG ATG	1587
Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met	
430 435 440	
CTT GTC GCA ATT CTA AAC ATC TGT ACT GAA GAT GAG CTG GAA AAC GAC	1635
Leu Val Ala Ile Leu Asn Ile Cys Thr Glu Asp Glu Leu Glu Asn Asp	
445 450 455	
ACC CCC GTC ATT GAA GAA TTA GTT GGT ACC GAT AAA AAA TTG CCA CAA	1683
Thr Pro Val Ile Glu Glu Leu Val Gly Thr Asp Lys Lys Leu Pro Gln	
460 465 470	
GCT GGT AAG TCG GAA GCA ACT CCA CAA CCA GCC ACT TCG GCG TCG CCT	1731
Ala Gly Lys Ser Glu Ala Thr Pro Gln Pro Ala Thr Ser Ala Ser Pro	
475 480 485 490	
AAA CAT GCT TCC ATT TTA GAT GAC GAA CAT CGA AGG AAA GCC TTA CGA	1779
Lys His Ala Ser Ile Leu Asp Asp Glu His Arg Arg Lys Ala Leu Arg	
495 500 505	
AAT AAG ATT CTG GCC GTC GCC AAA GTT TCC AGA ATG TAT TCT GTT CTC	1827
Asn Lys Ile Leu Ala Val Ala Lys Val Ser Arg Met Tyr Ser Val Leu	
510 515 520	
AGA GAA GAA ACC AAT AAA GTT CAG TTT TTA AAA GAT CAC AAT TCA GGC	1875
Arg Glu Glu Thr Asn Lys Val Gln Phe Leu Lys Asp His Asn Ser Gly	
525 530 535	
GTG TTG CCA CGT GGC GCT TTA TCT AAT GGT GTA AAG GGT TTA GAT GAA	1923
Val Leu Pro Arg Gly Ala Leu Ser Asn Gly Val Lys Gly Leu Asp Glu	
540 545 550	
GCC CTG TCT ACC TTT GAA AGG GCA AGA AAG CAC GAT TTA ATT AAT GAA	1971
Ala Leu Ser Thr Phe Glu Arg Ala Arg Lys His Asp Leu Ile Asn Glu	
555 560 565 570	
AAA TTA CCG CCT TCA CTA GAC GAA CTG AAA AAC GAA AAT AAG AAG TAC	2019
Lys Leu Pro Pro Ser Leu Asp Glu Leu Lys Asn Glu Asn Lys Lys Tyr	
575 580 585	
TAC GAA AAA GTT TGG CAG AAA GTA CAT GAA CAT GAT GCA AAG AAT GAT	2067
Tyr Glu Lys Val Trp Gln Lys Val His Glu His Asp Ala Lys Asn Asp	
590 595 600	
AGC AAA TAGAGAAAGC TCCTATTTCC ACTGTACATA CTTCAATAAG TAAGTAAGTT	2123
Ser Lys	
GCATTAATTA TCTATTTAGA AGCTAGATGC TCCTCAAATG CACAGAATCA TATAGCGTTT	2183
TATTAGGTCT GTTCTTTATT TTAGTTTTGT TGATCTCTAT GAAGGTATAT TTATATGCAA	2243
AAATAAACTT TTAAATATCT ATGGATGCTT ACTCAATTGT ATAGACGTTT TTCATAGGAG	2303
TGCAAATTAT GGACACCACC TTCTAATTGA GCAGAAGCGG TTCTGAATTC	2353

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 604 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Ser Ser Asp Ala Ile Arg Asn Thr Glu Gln Ile Asn Ala Ala Ile
 1           5           10           15
Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro Gln Ser Ser Thr Thr Pro
          20           25           30
Ile Asp Ser Lys Ala Ser Thr Val Ala Ala Ala Asn Ser Thr Ala Thr
          35           40           45
Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr Leu Asp Asp Gly Arg Val
          50           55           60
Val Ser Thr Asn Arg Arg Ile Met Asn Lys Val Pro Ala Ile Thr Ser
          65           70           75           80
His Val Pro Thr Asp Glu Glu Leu Phe Gln Pro Asn Gly Ile Pro Arg
          85           90           95
His Glu Phe Leu Arg Asp His Phe Lys Arg Glu Gly Lys Leu Ser Ala
          100          105          110
Ala Gln Ala Ala Arg Ile Val Thr Leu Ala Thr Glu Leu Phe Ser Lys
          115          120          125
Glu Pro Asn Leu Ile Ser Val Pro Ala Pro Ile Thr Val Cys Gly Asp
          130          135          140
Ile His Gly Gln Tyr Phe Asp Leu Leu Lys Leu Phe Glu Val Gly Gly
          145          150          155          160
Asp Pro Ala Thr Thr Ser Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
          165          170          175
Gly Ser Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr Ser Leu Lys Leu
          180          185          190
Asn Phe Asn Asp His Phe Trp Leu Leu Arg Gly Asn His Glu Cys Lys
          195          200          205
His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met Leu His Lys Tyr
          210          215          220
Asn Leu Asp Ile Tyr Glu Lys Cys Cys Glu Ser Phe Asn Asn Leu Pro
          225          230          235          240
Leu Ala Ala Leu Met Asn Gly Gln Tyr Leu Cys Val His Gly Gly Ile
          245          250          255
Ser Pro Glu Leu Asn Ser Leu Gln Asp Ile Asn Asn Leu Asn Arg Phe
          260          265          270
Arg Glu Ile Pro Ser His Gly Leu Met Cys Asp Leu Leu Trp Ala Asp
          275          280          285
Pro Ile Glu Glu Tyr Asp Glu Val Leu Asp Lys Asp Leu Thr Glu Glu
          290          295          300
Asp Ile Val Asn Ser Lys Thr Met Val Pro His His Gly Lys Met Ala
          305          310          315          320
Pro Ser Arg Asp Met Phe Val Pro Asn Ser Val Arg Gly Cys Ser Tyr
          325          330          335

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Ala	Phe	Thr	Tyr 340	Arg	Ala	Ala	Cys 345	His	Phe	Leu	Gln	Glu	Thr 350	Gly	Leu
Leu	Ser	Ile 355	Ile	Arg	Ala	His	Glu 360	Ala	Gln	Asp	Ala	Gly 365	Tyr	Arg	Met
Tyr	Lys 370	Asn	Thr	Lys	Thr	Leu 375	Gly	Phe	Pro	Ser	Leu 380	Leu	Thr	Leu	Phe
Ser 385	Ala	Pro	Asn	Tyr	Leu 390	Asp	Thr	Tyr	Asn	Asn 395	Lys	Ala	Ala	Ile	Leu 400
Lys	Tyr	Glu	Asn	Asn 405	Val	Met	Asn	Ile	Arg 410	Gln	Phe	Asn	Met	Thr 415	Pro
His	Pro	Tyr	Trp 420	Leu	Pro	Asp	Phe	Met 425	Asp	Val	Phe	Thr	Trp 430	Ser	Leu
Pro	Phe	Val 435	Gly	Glu	Lys	Val	Thr 440	Glu	Met	Leu	Val	Ala 445	Ile	Leu	Asn
Ile	Cys 450	Thr	Glu	Asp	Glu	Leu 455	Glu	Asn	Asp	Thr	Pro 460	Val	Ile	Glu	Glu
Leu 465	Val	Gly	Thr	Asp	Lys 470	Lys	Leu	Pro	Gln	Ala 475	Gly	Lys	Ser	Glu	Ala 480
Thr	Pro	Gln	Pro	Ala 485	Thr	Ser	Ala	Ser	Pro 490	Lys	His	Ala	Ser	Ile 495	Leu
Asp	Asp	Glu	His 500	Arg	Arg	Lys	Ala	Leu 505	Arg	Asn	Lys	Ile	Leu 510	Ala	Val
Ala	Lys	Val 515	Ser	Arg	Met	Tyr	Ser 520	Val	Leu	Arg	Glu	Glu 525	Thr	Asn	Lys
Val	Gln 530	Phe	Leu	Lys	Asp	His 535	Asn	Ser	Gly	Val	Leu 540	Pro	Arg	Gly	Ala
Leu 545	Ser	Asn	Gly	Val	Lys 550	Gly	Leu	Asp	Glu	Ala 555	Leu	Ser	Thr	Phe	Glu 560
Arg	Ala	Arg	Lys	His 565	Asp	Leu	Ile	Asn	Glu 570	Lys	Leu	Pro	Pro	Ser 575	Leu
Asp	Glu	Leu	Lys 580	Asn	Glu	Asn	Lys	Lys 585	Tyr	Tyr	Glu	Lys	Val 590	Trp	Gln
Lys	Val	His 595	Glu	His	Asp	Ala	Lys 600	Asn	Asp	Ser	Lys				

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 812 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

BNSDOCID: <WO\_\_9612806A1 | >

61

## CNB1 coding sequence

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 54..104

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 181..652

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTTGGAAC TCAATGGTGA TCAGAATCCA TAGAAGCATT TTTATTTCTT AAA ATG	56
Met	
1	
GGT GCT GCT CCT TCC AAA ATT GTG GAT GGT CTT TTA GAA GAT ACA AAT	104
Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr Asn	
5 10 15	
TGTATGTACA CTTCGGAGTG AGGAAAAGAA AGAAAGGGGA AATTAACCGA TTTTACTAAC	164
ACTGACACTT TGAACA GTT GAT AGA GAT GAA ATT GAA AGG TTA AGG AAG	213
Val Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys	
1 5 10	
AGA TTC ATG AAA TTA GAT AGA GAT AGC TCA GGG TCT ATT GAT AAA AAT	261
Arg Phe Met Lys Leu Asp Arg Asp Ser Gly Ser Ile Asp Lys Asn	
15 20 25	
GAA TTT ATG AGC ATT CCT GGC GTT TCG TCA AAC CCT CTT GCT GGA CGT	309
Glu Phe Met Ser Ile Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg	
30 35 40	
ATA ATG GAG GTT TTC GAT GCT GAT AAT AGT GGG GAC GTG GAT TTT CAA	357
Ile Met Glu Val Phe Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln	
45 50 55	
GAG TTC ATC ACA GGA TTA TCC ATT TTC AGT GGG CGT GGG TCC AAG GAC	405
Glu Phe Ile Thr Gly Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp	
60 65 70 75	
GAA AAG TTA AGA TTC GCC TTC AAA ATC TAC GAC ATT GAC AAG GAC GGT	453
Glu Lys Leu Arg Phe Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly	
80 85 90	
TTC ATA TCC AAT GGT GAG TTG TTC ATC GTG TTG AAG ATT ATG GTA GGT	501
Phe Ile Ser Asn Gly Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly	
95 100 105	
TCT AAT CTG GAC GAT GAA CAG CTG CAA CAG ATA GTA GAT AGG ACG ATA	549
Ser Asn Leu Asp Asp Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile	
110 115 120	
GTG GAA AAC GAT AGC GAC GGC GAC GGA CGT TTA AGT TTC GAG GAG TTT	597
Val Glu Asn Asp Ser Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe	
125 130 135	
AAG AAT GCT ATC GAA ACC ACA GAA GTG GCC AAG AGT CTG ACA TTG CAA	645
Lys Asn Ala Ile Glu Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln	
140 145 150 155	
TAC GATGTGTAAG ACTAGGGGAC ACTTCATTCA TTTATGGTAT GCCAATATTT	698
Tyr Asp	

TTAAGAAAAG AAGAATAATA CGCGATATTG TTTTAAAGG AAGGAACGCA CACTCGCCCA 758  
 GTTAGAGTGC TGATGATATA TACATATATA TATGTATATG TAACAAACAA TAAG 812

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr  
 1 5 10 15  
 Asn

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys Arg Phe Met Lys Leu  
 1 5 10 15  
 Asp Arg Asp Ser Ser Gly Ser Ile Asp Lys Asn Glu Phe Met Ser Ile  
 20 25 30  
 Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg Ile Met Glu Val Phe  
 35 40 45  
 Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln Glu Phe Ile Thr Gly  
 50 55 60  
 Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp Glu Lys Leu Arg Phe  
 65 70 75 80  
 Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly Phe Ile Ser Asn Gly  
 85 90 95  
 Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly Ser Asn Leu Asp Asp  
 100 105 110  
 Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile Val Glu Asn Asp Ser  
 115 120 125  
 Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe Lys Asn Ala Ile Glu  
 130 135 140  
 Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln Tyr Asp  
 145 150 155



## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: coding sequence of CNB1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..524

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GGT GCT GCT CCT TCC AAA ATT GTG GAT GGT CTT TTA GAA GAT ACA	48
Met Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr	
1 5 10 15	
AAT TTT GAT AGA GAT GAA ATT GAA AGG TTA AGG AAG AGA TTC ATG AAA	96
Asn Phe Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys Arg Phe Met Lys	
20 25 30	
TTA GAT AGA GAT AGC TCA GGG TCT ATT GAT AAA AAT GAA TTT ATG AGC	144
Leu Asp Arg Asp Ser Ser Gly Ser Ile Asp Lys Asn Glu Phe Met Ser	
35 40 45	
ATT CCT GGC GTT TCG TCA AAC CCT CTT GCT GGA CGT ATA ATG GAG GTT	192
Ile Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg Ile Met Glu Val	
50 55 60	
TTC GAT GCT GAT AAT AGT GGG GAC GTG GAT TTT CAA GAG TTC ATC ACA	240
Phe Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln Glu Phe Ile Thr	
65 70 75 80	
GGA TTA TCC ATT TTC AGT GGG CGT GGG TCC AAG GAC GAA AAG TTA AGA	288
Gly Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp Glu Lys Leu Arg	
85 90 95	
TTC GCC TTC AAA ATC TAC GAC ATT GAC AAG GAC GGT TTC ATA TCC AAT	336
Phe Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly Phe Ile Ser Asn	
100 105 110	
GGT GAG TTG TTC ATC GTG TTG AAG ATT ATG GTA GGT TCT AAT CTG GAC	384
Gly Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly Ser Asn Leu Asp	
115 120 125	
GAT GAA CAG CTG CAA CAG ATA GTA GAT AGG ACG ATA GTG GAA AAC GAT	432
Asp Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile Val Glu Asn Asp	
130 135 140	
AGC GAC GGC GAC GGA CGT TTA AGT TTC GAG GAG TTT AAG AAT GCT ATC	480
Ser Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe Lys Asn Ala Ile	
145 150 155 160	
GAA ACC ACA GAA GTG GCC AAG AGT CTG ACA TTG CAA TAC GAT GT	524
Glu Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln Tyr Asp	
165 170	

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

M t Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr
 1           5           10           15
Asn Phe Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys Arg Phe Met Lys
          20           25           30
Leu Asp Arg Asp Ser Ser Gly Ser Ile Asp Lys Asn Glu Phe Met Ser
          35           40           45
Ile Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg Ile Met Glu Val
          50           55           60
Phe Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln Glu Phe Ile Thr
          65           70           75           80
Gly Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp Glu Lys Leu Arg
          85           90           95
Phe Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly Phe Ile Ser Asn
          100          105          110
Gly Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly Ser Asn Leu Asp
          115          120          125
Asp Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile Val Glu Asn Asp
          130          135          140
Ser Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe Lys Asn Ala Ile
          145          150          155          160
Glu Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln Tyr Asp
          165          170

```

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: DNA fragment containing CNAIdeltaC coding sequence

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 286..1812

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTTGTTGCA TTTTGATATT CATCTATATC TATTTCAAAA TTTTTCATGT CATCGCCTCT	60
TGAAACATGA ATTTTCCAAT TCTGAAAAAG AACGTACTAC TGGGAAACAA AAGGGAAAAA	120
TGTATAAATC CTTTAATGTT TTTGAATCAA GAGGCATTAT TATAAAAGAA CGAAGCAAAG	180
CCTTTAATAT TTGCTTTATT AAAGGTATTA TTCAAAGAAA AGTTTTTTTA GATTCTTTTT	240
TTTTTGACGT ATTAGCTCAG CTGCCATAAA ACACCTCTCAA CGCCA ATG TCG AAA	294
Met Ser Lys	
1	
GAC TTG AAT TCT TCA CGC ATC AAA ATC ATT AAA CCT AAT GAC TCT TAC	342
Asp Leu Asn Ser Ser Arg Ile Lys Ile Ile Lys Pro Asn Asp Ser Tyr	
5 10 15	
ATA AAG GTT GAC CGG AAA AAA GAT TTA ACA AAA TAC GAA TTA GAA AAC	390
Ile Lys Val Asp Arg Lys Lys Asp Leu Thr Lys Tyr Glu Leu Glu Asn	
20 25 30 35	
GGT AAA GTA ATT TCT ACT AAG GAC CGA TCC TAC GCT TCT GTA CCT GCC	438
Gly Lys Val Ile Ser Thr Lys Asp Arg Ser Tyr Ala Ser Val Pro Ala	
40 45 50	
ATA ACA GGA AAG ATA CCA AGT GAT GAG GAA GTA TTC GAC TCC AAG ACG	486
Ile Thr Gly Lys Ile Pro Ser Asp Glu Glu Val Phe Asp Ser Lys Thr	
55 60 65	
GGA TTA CCT AAT CAT TCC TTT TTA AGA GAG CAT TTC TTT CAT GAG GGT	534
Gly Leu Pro Asn His Ser Phe Leu Arg Glu His Phe Phe His Glu Gly	
70 75 80	
CGA CTT TCT AAG GAA CAG GCC ATA AAA ATC TTA AAT ATG TCA ACT GTA	582
Arg Leu Ser Lys Glu Gln Ala Ile Lys Ile Leu Asn Met Ser Thr Val	
85 90 95	
GCA TTG AGT AAA GAA CCC AAT CTA CTA AAA CTC AAA GCG CCA ATT ACT	630
Ala Leu Ser Lys Glu Pro Asn Leu Leu Lys Leu Lys Ala Pro Ile Thr	
100 105 110 115	
ATA TGT GGT GAT ATT CAC GGG CAG TAT TAT GAT TTA TTG AAA CTG TTT	678
Ile Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu Lys Leu Phe	
120 125 130	
GAA GTT GGC GGT GAC CCC GCC GAA ATC GAC TAT TTA TTC TTG GGG GAT	726
Glu Val Gly Gly Asp Pro Ala Glu Ile Asp Tyr Leu Phe Leu Gly Asp	
135 140 145	
TAT GTT GAT AGA GGT GCA TTC TCT TTT GAG TGT CTG ATT TAT TTG TAC	774
Tyr Val Asp Arg Gly Ala Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr	
150 155 160	
TCC TTG AAG TTG AAT AAT TTA GGG AGA TTT TGG ATG CTA AGA GGT AAC	822
Ser Leu Lys Leu Asn Asn Leu Gly Arg Phe Trp Met Leu Arg Gly Asn	
165 170 175	
CAT GAG TGT AAG CAC TTG ACC TCT TAT TTT ACT TTT AAG AAT GAG ATG	870
His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met	
180 185 190 195	
TTG CAC AAA TAC GAT ATG GAA GTT TAC GAT GCT TGC TGC AGA TCA TTC	918
Leu His Lys Tyr Asp Met Glu Val Tyr Asp Ala Cys Cys Arg S r Phe	
200 205 210	

66

AAT GTC TTA CCA TTA GCA GCT TTA ATG AAC GGA CAA TAT TTT TGT GTG	966
Asn Val Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr Phe Cys Val	
215 220 225	
CAT GGT GGT ATC TCT CCA GAG TTA AAA TCA GTA GAG GAT GTT AAT AAA	1014
His Gly Gly Ile Ser Pro Glu Leu Lys Ser Val Glu Asp Val Asn Lys	
230 235 240	
ATT AAT AGA TTT CGA GAA ATC CCA TCT CGT GGT CTC ATG TGT GAC CTA	1062
Il Asn Arg Phe Arg Glu Ile Pro Ser Arg Gly Leu Met Cys Asp Leu	
245 250 255	
CTA TGG GCC GAT CCT GTC GAA AAT TAT GAT GAT GCA AGA GAT GGT AGC	1110
Leu Trp Ala Asp Pro Val Glu Asn Tyr Asp Asp Ala Arg Asp Gly Ser	
260 265 270 275	
GAA TTT GAT CAG AGC GAG GAT GAA TTC GTA CCT AAC AGT TTG AGG GGT	1158
Glu Phe Asp Gln Ser Glu Asp Glu Phe Val Pro Asn Ser Leu Arg Gly	
280 285 290	
TGC TCT TTC GCC TTC ACT TTT AAA GCA TCA TGC AAG TTT TTG AAG GCA	1206
Cys Ser Phe Ala Phe Thr Phe Lys Ala Ser Cys Lys Phe Leu Lys Ala	
295 300 305	
AAT GGT TTG TTA TCT ATT ATT AGA GCA CAC GAA GCA CAG GAT GCT GGG	1254
Asn Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly	
310 315 320	
TAC AGA ATG TAT AAA AAC AAT AAA GTA ACA GGC TTC CCG AGC TTA ATA	1302
Tyr Arg Met Tyr Lys Asn Asn Lys Val Thr Gly Phe Pro Ser Leu Ile	
325 330 335	
ACC ATG TTC AGT GCG CCA AAC TAC CTG GAC ACA TAT CAT AAT AAA GCT	1350
Thr Met Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr His Asn Lys Ala	
340 345 350 355	
GCT GTG TTA AAA TAT GAA GAA AAC GTC ATG AAC ATC AGG CAG TTT CAC	1398
Ala Val Leu Lys Tyr Glu Glu Asn Val Met Asn Ile Arg Gln Phe His	
360 365 370	
ATG TCT CCG CAC CCT TAC TGG TTG CCT GAT TTT ATG GAT GTT TTC ACC	1446
Met Ser Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp Val Phe Thr	
375 380 385	
TGG TCA CTA CCT TTT GTT GGC GAA AAA GTT ACT AGC ATG TTA GTG TCT	1494
Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Ser Met Leu Val Ser	
390 395 400	
ATA TTA AAC ATA TGT AGT GAG CAG GAA CTT GAC CCA GAA TCG GAA CCC	1542
Ile Leu Asn Ile Cys Ser Glu Gln Glu Leu Asp Pro Glu Ser Glu Pro	
405 410 415	
AAA GCT GCG GAG GAG ACT GTA AAG GCA AGA GCA AAC GCA ACT AAG GAG	1590
Lys Ala Ala Glu Glu Thr Val Lys Ala Arg Ala Asn Ala Thr Lys Glu	
420 425 430 435	
ACC GGC ACC CCA TCT GAT GAA AAG GCG TCA TCA GCG ATA TTA GAA GAT	1638
Thr Gly Thr Pro Ser Asp Glu Lys Ala Ser Ser Ala Ile Leu Glu Asp	
440 445 450	
GAA ACC CGA AGA AAG GCT TTG AGA AAT AAG ATA TTA GCT ATT GCT AAA	1686
Glu Thr Arg Arg Lys Ala Leu Arg Asn Lys Ile Leu Ala Ile Ala Lys	
455 460 465	
GTT TCA AGA ATG TTT TCG GTG CTA AGA GAA GAG AGC GAA AAA GTG GAA	1734
Val Ser Arg Met Phe Ser Val Leu Arg Glu Glu Ser Glu Lys Val Glu	
470 475 480	

67

TAT TTG AAA ACT ATG AAT GCC GGT GTC TTA CCT CGT GGT GCT CTA GCT 1782  
 Tyr Leu Lys Thr Met Asn Ala Gly Val Leu Pro Arg Gly Ala Leu Ala  
 485 490 495

CGT GGG ACT GAA GGT TTG AAT GAA ACG CTA 1812  
 Arg Gly Thr Glu Gly Leu Asn Glu Thr Leu  
 500 505

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ser Lys Asp Leu Asn Ser Ser Arg Ile Lys Ile Ile Lys Pro Asn  
 1 5 10 15  
 Asp Ser Tyr Ile Lys Val Asp Arg Lys Lys Asp Leu Thr Lys Tyr Glu  
 20 25 30  
 Leu Glu Asn Gly Lys Val Ile Ser Thr Lys Asp Arg Ser Tyr Ala Ser  
 35 40 45  
 Val Pro Ala Ile Thr Gly Lys Ile Pro Ser Asp Glu Glu Val Phe Asp  
 50 55 60  
 Ser Lys Thr Gly Leu Pro Asn His Ser Phe Leu Arg Glu His Phe Phe  
 65 70 75 80  
 His Glu Gly Arg Leu Ser Lys Glu Gln Ala Ile Lys Ile Leu Asn Met  
 85 90 95  
 Ser Thr Val Ala Leu Ser Lys Glu Pro Asn Leu Leu Lys Leu Lys Ala  
 100 105 110  
 Pro Ile Thr Ile Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu  
 115 120 125  
 Lys Leu Phe Glu Val Gly Gly Asp Pro Ala Glu Ile Asp Tyr Leu Phe  
 130 135 140  
 L u Gly Asp Tyr Val Asp Arg Gly Ala Phe Ser Phe Glu Cys Leu Ile  
 145 150 155 160  
 Tyr Leu Tyr Ser Leu Lys Leu Asn Asn Leu Gly Arg Phe Trp Met Leu  
 165 170 175  
 Arg Gly Asn His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys  
 180 185 190  
 Asn Glu Met Leu His Lys Tyr Asp Met Glu Val Tyr Asp Ala Cys Cys  
 195 200 205  
 Arg Ser Phe Asn Val Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr  
 210 215 220  
 Phe Cys Val His Gly Gly Ile Ser Pro Glu Leu Lys Ser Val Glu Asp  
 225 230 235 240  
 Val Asn Lys Ile Asn Arg Phe Arg Glu Ile Pro Ser Arg Gly Leu Met  
 245 250 255

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1767 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(C) INDIVIDUAL ISOLATE: DNA fragment containing CNA2deltaC coding sequence

BNSDOCID: &lt;WO\_9612806A1\_1&gt;

(A) NAME/KEY: CDS  
(B) LOCATION: 262..1767

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGTCTATA ATACGTTTGA TACAGCTAGA TATCGCTAGC GCCAACATTG TCCCCCTCTC	60
TTGATCAATG CTTTTTTTCG GCCCGAGACA AATGAGAAAA TGTCCTAAAA ATACCTTTCA	120
TCAAGACTCC TATTTTTCCT TAGAAAAAAC ATATATCCAA CTGGAACAGT ATTAAGCCAA	180
TTGCTACGAT ACAAACAAAA GGAGATATTC CTTCCCTCCC ATAGAGTCAC ACAGGAGCCA	240
GTACTTCTTC TTGAACCCGC A ATG TCT TCA GAC GCT ATA AGA AAT ACT GAG	291
Met Ser Ser Asp Ala Ile Arg Asn Thr Glu	
1 5 10	
CAG ATA AAC GCC GCT ATT AAA ATT ATA GAA AAC AAA ACA GAG CGT CCG	339
Gln Ile Asn Ala Ala Ile Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro	
15 20 25	
CAA TCG TCC ACA ACC CCT ATA GAT TCG AAG GCT AGT ACA GTT GCT GCT	387
Gln Ser Ser Thr Thr Pro Ile Asp Ser Lys Ala Ser Thr Val Ala Ala	
30 35 40	
GCT AAT TCC ACG GCC ACA GAA ACT TCC AGA GAC CTT ACA CAA TAT ACC	435
Ala Asn Ser Thr Ala Thr Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr	
45 50 55	
CTA GAT GAC GGA AGA GTC GTA TCG ACA AAC CGC AGA ATA ATG AAT AAA	483
Leu Asp Asp Gly Arg Val Val Ser Thr Asn Arg Arg Ile Met Asn Lys	
60 65 70	
GTG CCC GCC ATC ACG TCA CAT GTT CCT ACA GAT GAA GAG CTG TTC CAG	531
Val Pro Ala Ile Thr Ser His Val Pro Thr Asp Glu Glu Leu Phe Gln	
75 80 85 90	
CCC AAT GGG ATA CCT CGT CAC GAA TTC CTA AGA GAT CAT TTC AAG CGC	579
Pro Asn Gly Ile Pro Arg His Glu Phe Leu Arg Asp His Phe Lys Arg	
95 100 105	
GAG GGC AAA TTG TCG GCT GCG CAG GCG GCC AGG ATC GTT ACA CTT GCA	627
Glu Gly Lys Leu Ser Ala Ala Gln Ala Ala Arg Ile Val Thr Leu Ala	
110 115 120	
ACG GAA CTC TTC AGC AAA GAA CCC AAC CTT ATA TCT GTT CCC GCC CCA	675
Thr Glu Leu Phe Ser Lys Glu Pro Asn Leu Ile Ser Val Pro Ala Pro	
125 130 135	
ATC ACA GTT TGC GGT GAT ATC CAT GGC CAG TAC TTT GAC CTT TTG AAG	723
Ile Thr Val Cys Gly Asp Ile His Gly Gln Tyr Phe Asp Leu Leu Lys	
140 145 150	
CTA TTC GAA GTT GGC GGA GAT CCG GCC ACT ACA TCG TAT TTG TTC TTG	771
Leu Phe Glu Val Gly Gly Asp Pro Ala Thr Thr Ser Tyr Leu Phe Leu	
155 160 165 170	
GGA GAC TAT GTC GAC AGA GGG TCC TTT TCG TTT GAG TGT CTT ATT TAT	819
Gly Asp Tyr Val Asp Arg Gly Ser Phe Ser Phe Glu Cys Leu Ile Tyr	
175 180 185	
TTA TAT TCT TTG AAG CTG AAT TTT AAC GAC CAT TTC TGG CTA CTG AGG	867
Leu Tyr Ser Leu Lys Leu Asn Phe Asn Asp His Phe Trp Leu Leu Arg	
190 195 200	

70

GGT	AAC	CAC	GAA	TGT	AAG	CAT	CTA	ACG	TCA	TAT	TTC	ACT	TTC	AAA	AAT	915
Gly	Asn	His	Glu	Cys	Lys	His	Leu	Thr	Ser	Tyr	Phe	Thr	Phe	Lys	Asn	
		205					210					215				
GAA	ATG	CTG	CAC	AAG	TAC	AAT	CTA	GAT	ATT	TAC	GAG	AAA	TGC	TGC	GAA	963
Glu	Met	Leu	His	Lys	Tyr	Asn	Leu	Asp	Ile	Tyr	Glu	Lys	Cys	Cys	Glu	
	220					225					230					
TCG	TTT	AAC	AAC	TTG	CCC	CTG	GCT	GCG	TTA	ATG	AAC	GGA	CAG	TAT	CTT	1011
Ser	Phe	Asn	Asn	Leu	Pro	Leu	Ala	Ala	Leu	Met	Asn	Gly	Gln	Tyr	Leu	
235					240					245					250	
TGT	GTT	CAT	GGT	GGT	ATA	TCT	CCC	GAG	TTA	AAC	TCT	TTA	CAG	GAC	ATT	1059
Cys	Val	His	Gly	Gly	Ile	Ser	Pro	Glu	Leu	Asn	Ser	Leu	Gln	Asp	Ile	
			255						260					265		
AAC	AAC	CTA	AAT	AGA	TTC	AGG	GAG	ATT	CCC	TCT	CAT	GGC	CTG	ATG	TGT	1107
Asn	Asn	Leu	Asn	Arg	Phe	Arg	Glu	Ile	Pro	Ser	His	Gly	Leu	Met	Cys	
		270						275					280			
GAT	CTG	TTG	TGG	GCT	GAC	CCG	ATT	GAA	GAG	TAC	GAC	GAA	GTC	TTG	GAT	1155
Asp	Leu	Leu	Trp	Ala	Asp	Pro	Ile	Glu	Glu	Tyr	Asp	Glu	Val	Leu	Asp	
	285						290					295				
AAA	GAC	TTG	ACT	GAG	GAA	GAC	ATA	GTG	AAC	TCC	AAA	ACC	ATG	GTT	CCT	1203
Lys	Asp	Leu	Thr	Glu	Glu	Asp	Ile	Val	Asn	Ser	Lys	Thr	Met	Val	Pro	
	300					305					310					
CAT	CAT	GGC	AAG	ATG	GCA	CCT	TCA	AGG	GAT	ATG	TTT	GTC	CCA	AAC	TCA	1251
His	His	Gly	Lys	Met	Ala	Pro	Ser	Arg	Asp	Met	Phe	Val	Pro	Asn	Ser	
315					320					325					330	
GTA	AGG	GGC	TGT	TCA	TAT	GCC	TTC	ACG	TAT	CGT	GCT	GCG	TGC	CAT	TTT	1299
Val	Arg	Gly	Cys	Ser	Tyr	Ala	Phe	Thr	Tyr	Arg	Ala	Ala	Cys	His	Phe	
			335						340					345		
CTG	CAA	GAG	ACT	GGC	CTG	TTG	TCC	ATC	ATC	AGG	GCA	CAC	GAG	GCT	CAA	1347
Leu	Gln	Glu	Thr	Gly	Leu	Leu	Ser	Ile	Ile	Arg	Ala	His	Glu	Ala	Gln	
			350					355					360			
GAC	GCT	GGT	TAT	AGA	ATG	TAC	AAA	AAT	ACC	AAG	ACT	TTG	GGC	TTT	CCC	1395
Asp	Ala	Gly	Tyr	Arg	Met	Tyr	Lys	Asn	Thr	Lys	Thr	Leu	Gly	Phe	Pro	
	365						370					375				
TCT	CTT	TTG	ACC	CTT	TTC	AGT	GCG	CCT	AAC	TAC	TTG	GAC	ACC	TAC	AAT	1443
Ser	Leu	Leu	Thr	Leu	Phe	Ser	Ala	Pro	Asn	Tyr	Leu	Asp	Thr	Tyr	Asn	
	380					385					390					
AAT	AAG	GCT	GCC	ATA	TTG	AAA	TAC	GAA	AAT	AAT	GTT	ATG	AAT	ATC	AGA	1491
Asn	Lys	Ala	Ala	Ile	Leu	Lys	Tyr	Glu	Asn	Asn	Val	Met	Asn	Ile	Arg	
395					400					405					410	
CAA	TTC	AAC	ATG	ACT	CCA	CAC	CCC	TAT	TGG	TTA	CCA	GAT	TTC	ATG	GAC	1539
Gln	Phe	Asn	Met	Thr	Pro	His	Pro	Tyr	Trp	Leu	Pro	Asp	Phe	Met	Asp	
			415						420					425		
GTT	TTC	ACG	TGG	TCC	TTG	CCA	TTT	GTT	GGT	GAA	AAA	GTT	ACA	GAG	ATG	1587
Val	Phe	Thr	Trp	Ser	Leu	Pro	Phe	Val	Gly	Glu	Lys	Val	Thr	Glu	Met	
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CTT	GTC	GCA	ATT	CTA	AAC	ATC	TGT	ACT	GAA	GAT	GAG	CTG	GAA	AAC	GAC	1635
Leu	Val	Ala	Ile	Leu	Asn	Ile	Cys	Thr	Glu	Asp	Glu	Leu	Glu	Asn	Asp	
		445					450					455				
ACC	CCC	GTC	ATT	GAA	GAA	TTA	GTT	GGT	ACC	GAT	AAA	AAA	TTG	CCA	CAA	1683
Thr	Pro	Val	Ile	Glu	Glu	Leu	Val	Gly	Thr	Asp	Lys	Lys	Leu	Pro	Gln	
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71

GCT GGT AAG TCG GAA GCA ACT CCA CAA CCA GCC ACT TCG GCG TCG CCT 1731  
 Ala Gly Lys Ser Glu Ala Thr Pro Gln Pro Ala Thr Ser Ala Ser Pro  
 475 480 485 490

AAA CAT GCT TCC ATT TTA GAT GAC GAA CAT CGA AGG 1767  
 Lys His Ala Ser Ile Leu Asp Asp Glu His Arg Arg  
 495 500

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ser Ser Asp Ala Ile Arg Asn Thr Glu Gln Ile Asn Ala Ala Ile  
 1 5 10 15  
 Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro Gln Ser Ser Thr Thr Pro  
 20 25 30  
 Ile Asp Ser Lys Ala Ser Thr Val Ala Ala Ala Asn Ser Thr Ala Thr  
 35 40 45  
 Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr Leu Asp Asp Gly Arg Val  
 50 55 60  
 Val Ser Thr Asn Arg Arg Ile Met Asn Lys Val Pro Ala Ile Thr Ser  
 65 70 75 80  
 His Val Pro Thr Asp Glu Glu Leu Phe Gln Pro Asn Gly Ile Pro Arg  
 85 90 95  
 His Glu Phe Leu Arg Asp His Phe Lys Arg Glu Gly Lys Leu Ser Ala  
 100 105 110  
 Ala Gln Ala Ala Arg Ile Val Thr Leu Ala Thr Glu Leu Phe Ser Lys  
 115 120 125  
 Glu Pro Asn Leu Ile Ser Val Pro Ala Pro Ile Thr Val Cys Gly Asp  
 130 135 140  
 Ile His Gly Gln Tyr Phe Asp Leu Leu Lys Leu Phe Glu Val Gly Gly  
 145 150 155 160  
 Asp Pro Ala Thr Thr Ser Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg  
 165 170 175  
 Gly Ser Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr Ser Leu Lys Leu  
 180 185 190  
 Asn Phe Asn Asp His Phe Trp Leu Leu Arg Gly Asn His Glu Cys Lys  
 195 200 205  
 His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met Leu His Lys Tyr  
 210 215 220  
 Asn Leu Asp Ile Tyr Glu Lys Cys Cys Glu Ser Phe Asn Asn Leu Pro  
 225 230 235 240  
 Leu Ala Ala Leu Met Asn Gly Gln Tyr Leu Cys Val His Gly Gly Ile  
 245 250 255

72

S r Pro Glu Leu Asn Ser L u Gln Asp Ile Asn Asn Leu Asn Arg Phe  
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 275 280 285  
 Pro Ile Glu Glu Tyr Asp Glu Val Leu Asp Lys Asp Leu Thr Glu Glu  
 290 295 300  
 Asp Ile Val Asn Ser Lys Thr Met Val Pro His His Gly Lys Met Ala  
 305 310 315 320  
 Pro Ser Arg Asp Met Phe Val Pro Asn Ser Val Arg Gly Cys Ser Tyr  
 325 330 335  
 Ala Phe Thr Tyr Arg Ala Ala Cys His Phe Leu Gln Glu Thr Gly Leu  
 340 345 350  
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 Tyr Lys Asn Thr Lys Thr Leu Gly Phe Pro Ser Leu Leu Thr Leu Phe  
 370 375 380  
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 385 390 395 400  
 Lys Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Met Thr Pro  
 405 410 415  
 His Pro Tyr Trp Leu Pro Asp Phe Met Asp Val Phe Thr Trp Ser Leu  
 420 425 430  
 Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Ala Ile Leu Asn  
 435 440 445  
 Ile Cys Thr Glu Asp Glu Leu Glu Asn Asp Thr Pro Val Ile Glu Glu  
 450 455 460  
 Leu Val Gly Thr Asp Lys Lys Leu Pro Gln Ala Gly Lys Ser Glu Ala  
 465 470 475 480  
 Thr Pro Gln Pro Ala Thr Ser Ala Ser Pro Lys His Ala Ser Ile Leu  
 485 490 495  
 Asp Asp Glu His Arg Arg  
 500

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: G4-PCR-A

73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCCTATCGT GCACTCACCG ACGC

24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G4-PCR-B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGAAGGCC C TACTGAGCCA GGAG

24

## IT IS CLAIMED:

1. A polypeptide composition comprising a polypeptide effective to enhance immunosuppressive effects of a calcineurin-targeted immunosuppressant by potentiating an interaction of an immunophilin with calcineurin.
2. A composition of claim 1, wherein the polypeptide composition contains a calcineurin interacting (CNI) polypeptide.
3. A composition of claim 2, wherein the polypeptide composition contains a polypeptide having an amino acid sequence selected from the group consisting of sequences represented by SEQ ID NO:2 and SEQ ID NO:5.
4. A composition of claim 2, wherein the polypeptide has an amino acid sequence of between 15 and 915 amino acids in length.
5. A composition of claim 2, wherein the polypeptide composition contains a polypeptide having an amino acid sequence comprising the c-terminal 306 amino acids of a CNI protein.
6. An isolated nucleic acid having a sequence encoding a polypeptide of any of claims 1-5.
7. A nucleic acid of claim 6, wherein the nucleic acid has a sequence selected from the group consisting of nucleic acid sequences represented by SEQ ID NO:3 and SEQ ID NO:6.
8. A method of identifying a small molecule immunosuppressant compound, comprising constructing a cell-based two hybrid protein-protein interaction assay, wherein one of two fusion hybrid proteins in a cell contains an (A) subunit of calcineurin, and the other of two fusion hybrid proteins contains a CNI polypeptide, contacting the cell with a small molecule, and

identifying the small molecule as an immunosuppressant if the molecule potentiates an interaction between the two hybrid proteins.

9. A method of claim 8, wherein the cell is a yeast cell.

5

10. A method of claim 8, wherein one of the two fusion hybrid proteins contains a GAL4 activation domain and the other of two fusion hybrid proteins contains a GAL4 binding domain.

10 11. A method of claim 8, wherein the subunit of calcineurin is selected from the group consisting of yeast CNA1 and yeast CNA2.

12. A method of claim 8, wherein the subunit of calcineurin is an "A" subunit of human calcineurin.

15

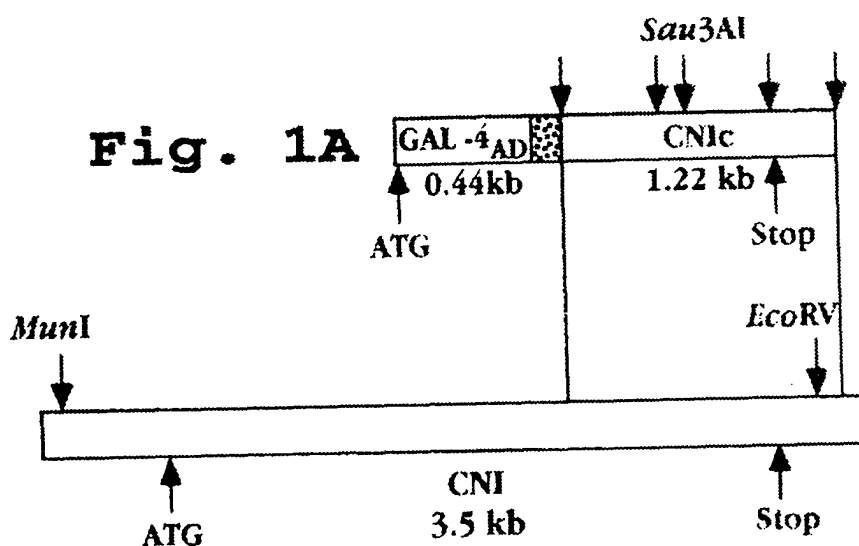
13. A method of claim 8, wherein the CNI polypeptide is yeast CNI polypeptide.

14. A method of claim 8, wherein the CNI polypeptide is yeast CN1c polypeptide.

20 15. A method of claim 8, wherein the cell is further modified to cause overexpression of a "B" subunit of calcineurin by said cell.

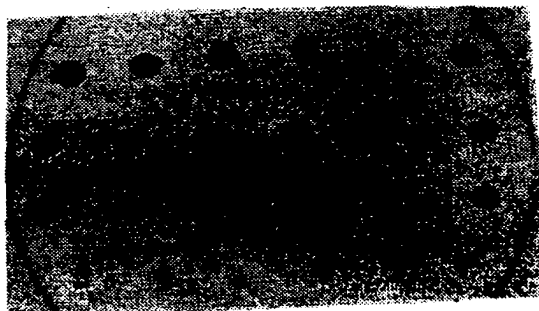
25 16. A yeast cell carrying a mutation in the naturally-occurring genomic copy of a gene encoding calcineurin-interacting polypeptide, where said mutation prevents expression of a functional calcineurin-interacting polypeptide from said genomic copy.

1/11

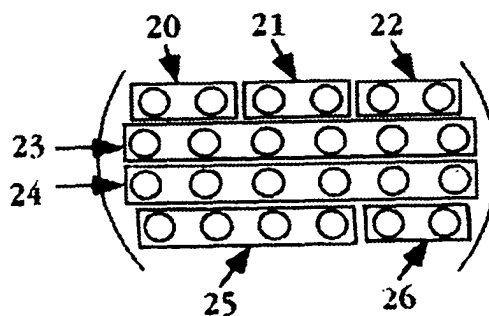


**Fig. 1B**

**Fig. 2A**

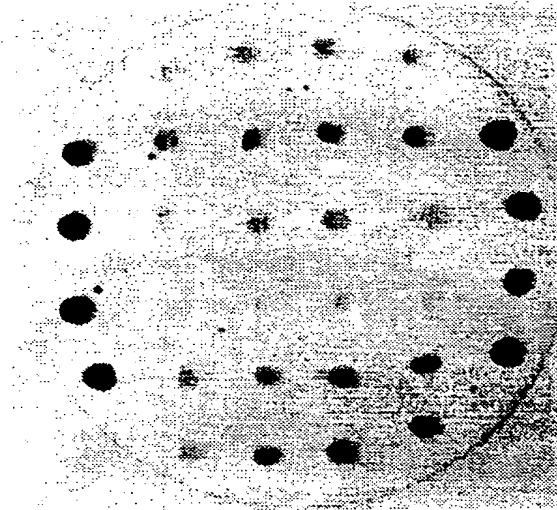


**Fig. 2B**

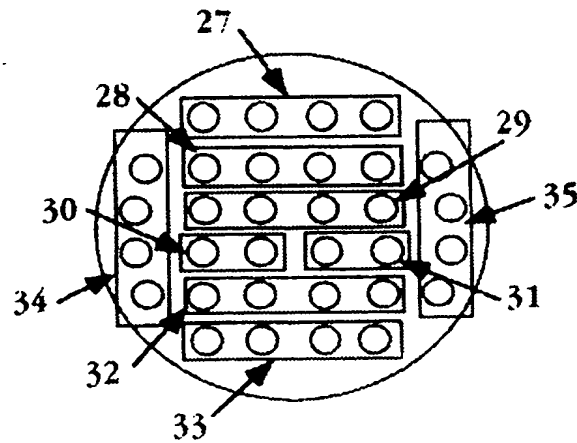


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2/11

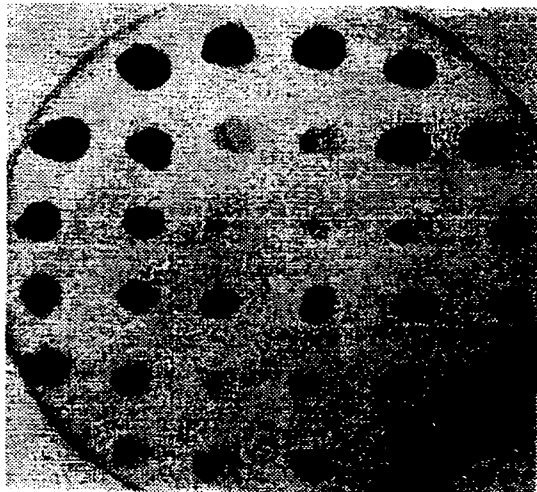


**Fig. 3A**

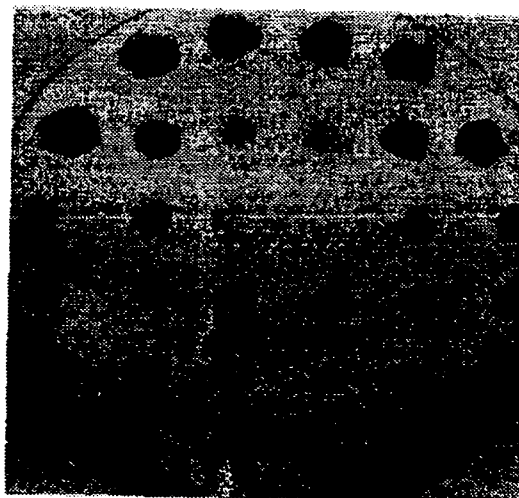


**Fig. 3B**

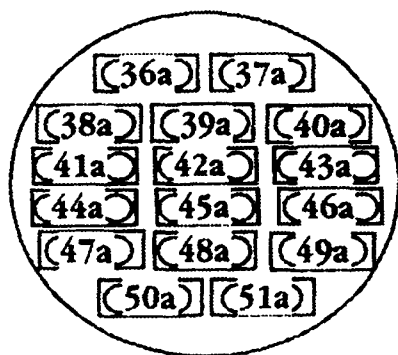
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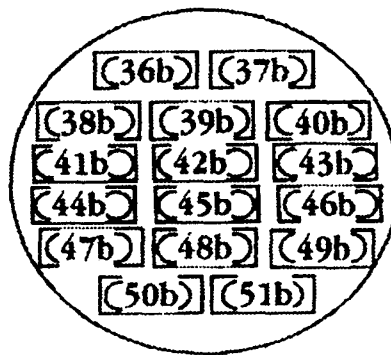
**Fig. 4A**



**Fig. 4C**



**Fig. 4B**

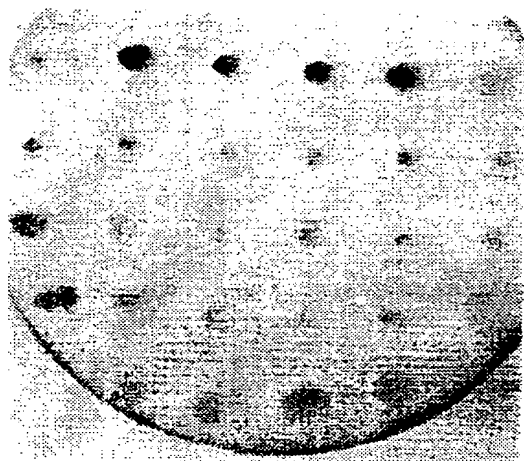


**Fig. 4D**

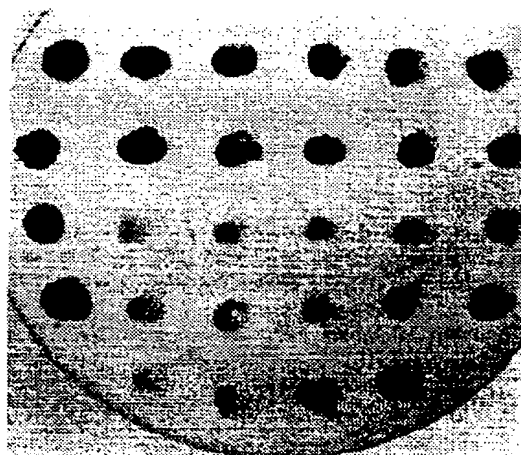
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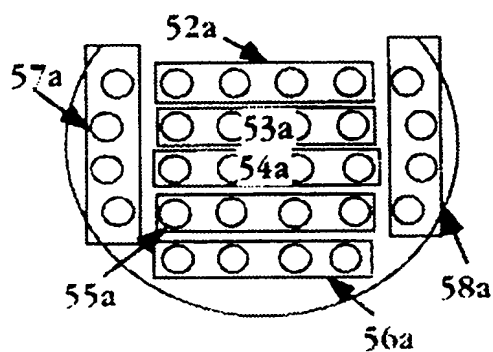
4/11



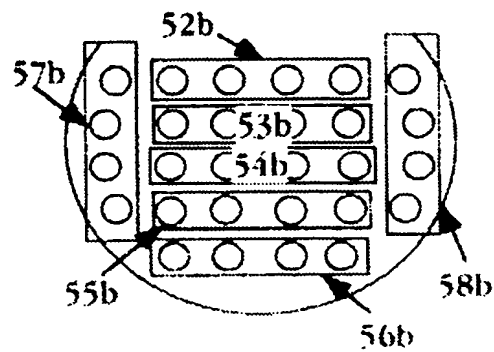
**Fig. 5A**



**Fig. 5C**



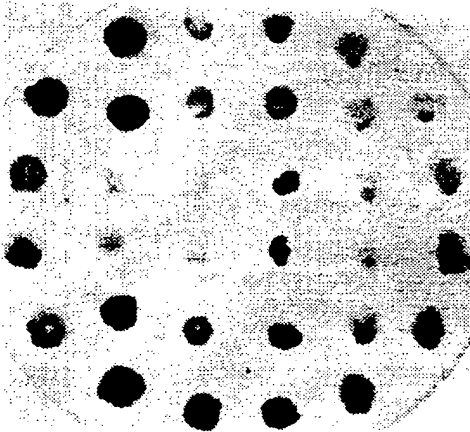
**Fig. 5B**



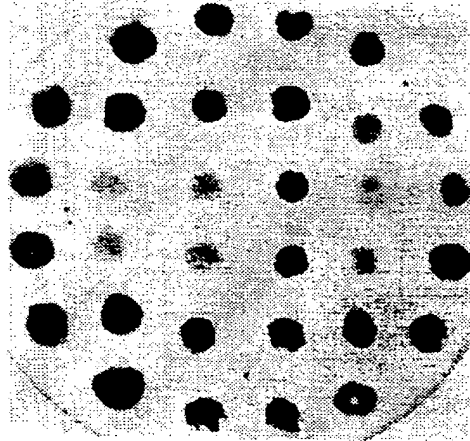
**Fig. 5D**

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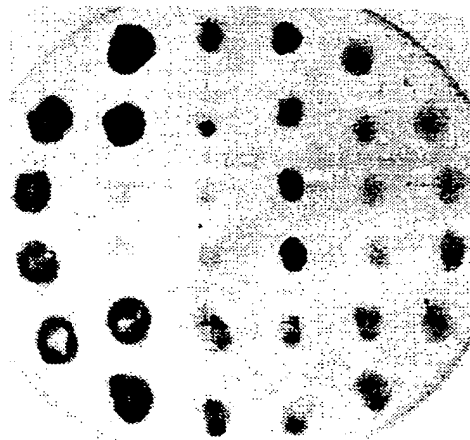
5/11



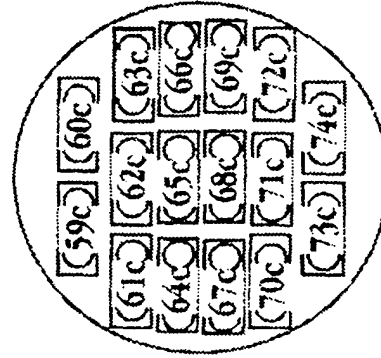
**Fig. 6E**



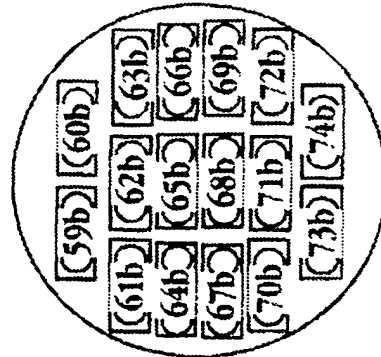
**Fig. 6C**



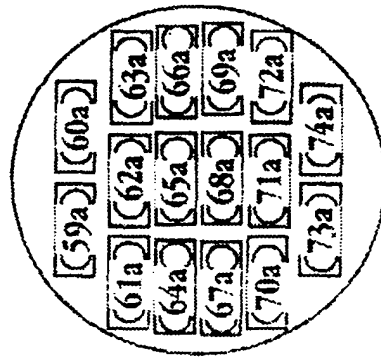
**Fig. 6A**



**Fig. 6F**



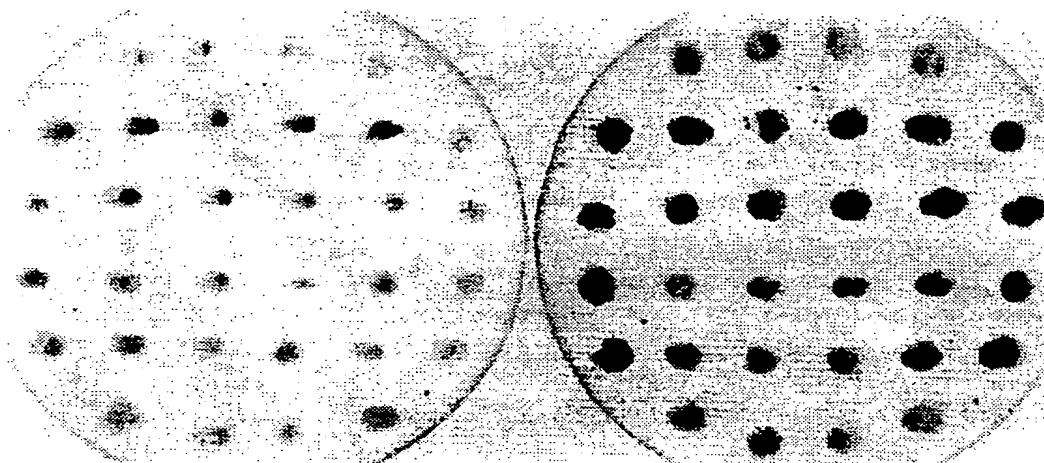
**Fig. 6D**



**Fig 6B**

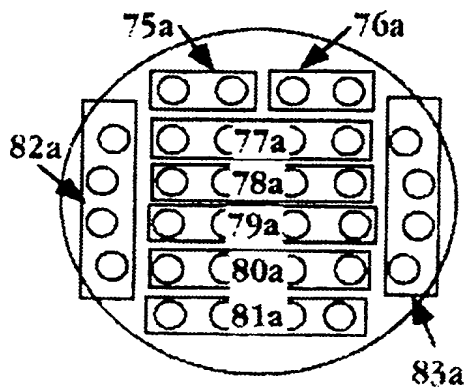
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6/11

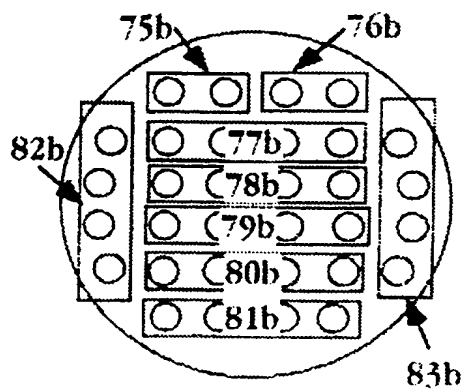


**Fig. 7A**

**Fig. 7C**

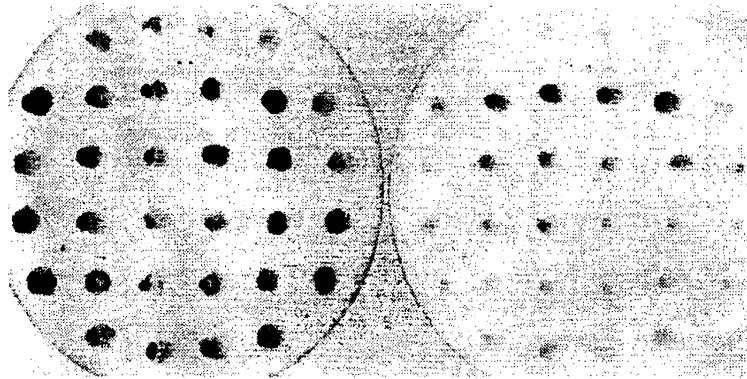


**Fig. 7B**



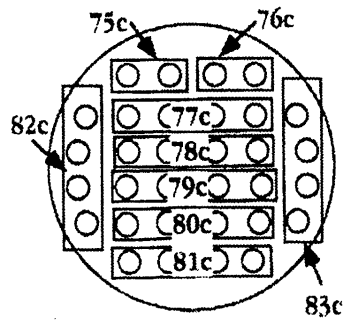
**Fig. 7D**

**SUBSTITUTE SHEET (RULE 26)**

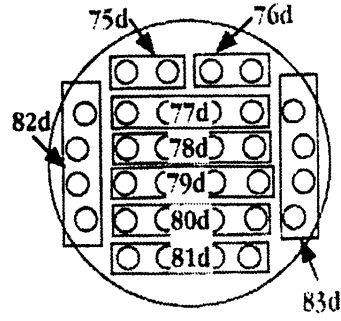


**Fig. 7E**

**Fig. 7G**

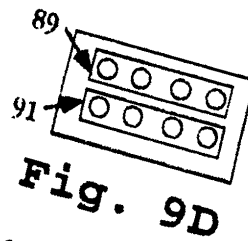
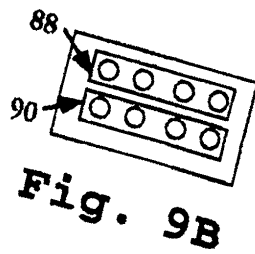
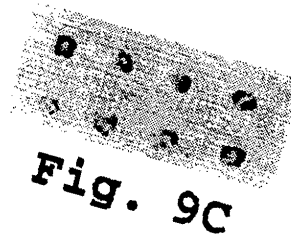
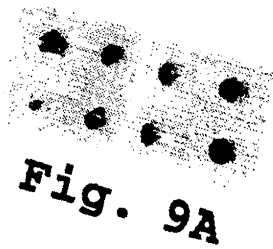
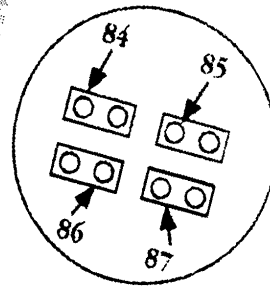
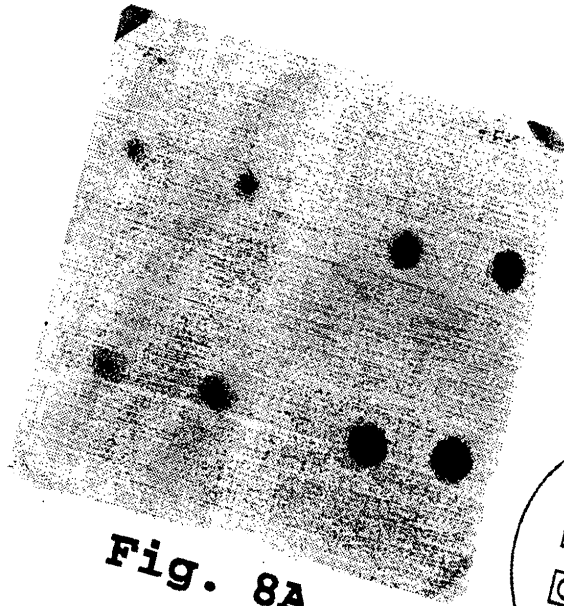


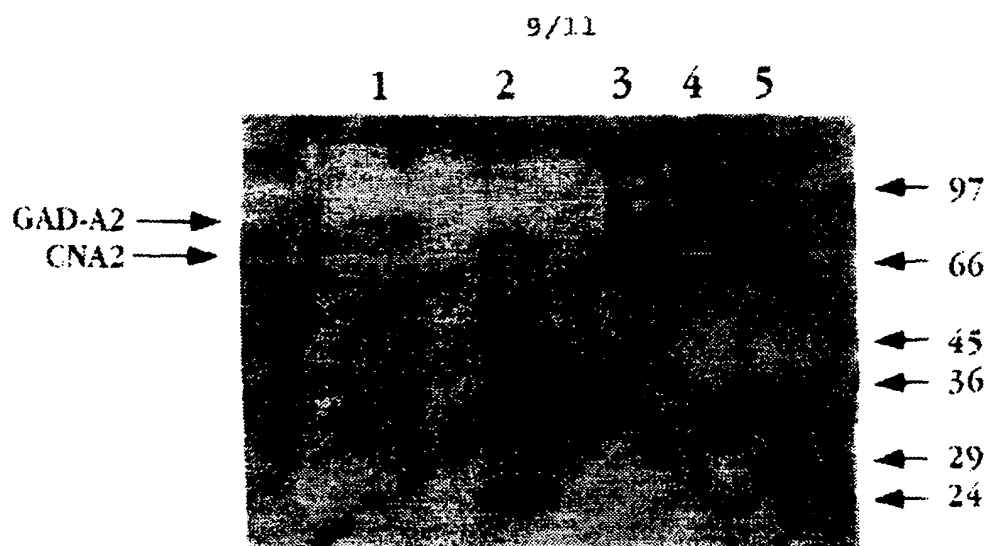
**Fig. 7F**



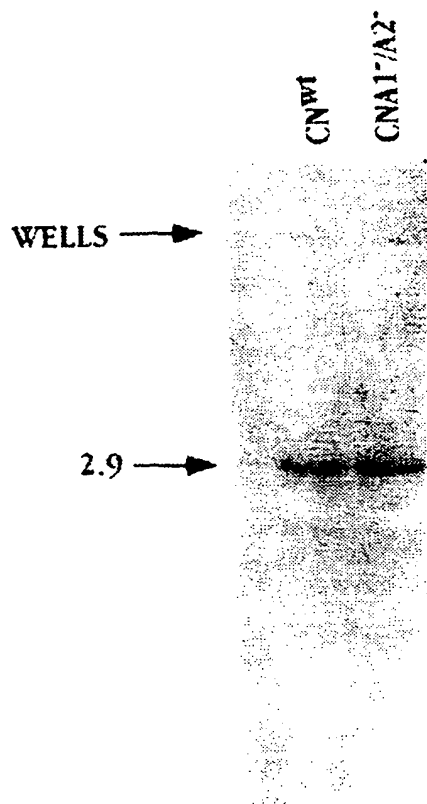
**Fig. 7H**

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**Fig. 10**



**Fig. 11**

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10/11

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Fig. 12

11/11

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PILNYQPLSNSPPPDDFDLAKRGAADSHAIPVDPPSYFDVLKADGIELPYDTSSSKIPELKLNKSRETLA  
SIEEDSFNGWSQIDDLSDEDDNDGDIASGFNFKLSTSAPSENVNSHTPILQSLNMSLDGRKKNRASLHATSV  
LPSTIRQNNQHFNDINQMLGSSDEDAFPKSQSLNFNKKLPILKINDNVIQSNSNSNNRVDPEDTVDSSVDI  
TAFYDPRMSSDSKFDWEVSKNHVDPAAYSVNVASENRVLDDFKKAFREKRK

**Fig. 13**



## IN NATIONAL SEARCH REPORT

International Application No

PCT/US 95/13580

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/395 G01N33/68 C12N15/62 C12Q1/00  
C12N1/16 //(C12N1/16,C12R1:865)

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Swissprot Database entry YK01_YEAST Accession number P36117; June 01, 1994 Duesterhoeft A. et al.: 'Hypothetical 102.5 kD protein in YPT52-GCN3 intergenic region.'	1-5
X	Emfun Database entry Scykr021w Accession number Z28246; May 10, 1994 Duesterhoeft A. et al.: 'S. cerevisiae chromosome XI reading frame ORF YKR021w.'	6,7
P,X	MOLECULAR BIOLOGY OF THE CELL, 5 (SUPPL.). 1994. 141A., HUANG L ET AL 'A novel protein that interacts with calcineurin in vivo' see abstract 818	1,2,6, 8-15



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

## \* Special categories of cited documents:

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- 'Y' document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- '&' document member of the same patent family

Date of the actual completion of the international search

21 March 1996

Date of mailing of the international search report

02.04.96

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# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 95/13580

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>CURR BIOL, 2 (1). 1992. 18-20., CYERT M S 'IMMUNOSUPPRESSANTS HIT THE TARGET' see the whole document -----</p>	